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2: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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US-09-651-200-2
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US-09-610-174B-18
US-09-620-461-18
US-09-910-174B-15
US-09-910-174B-16
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US-09-910-174B-14
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	ALIGNMENTS	US-08-724-394A-3	US-09-620-461-11	US-09-910-174B-11	US-08-724-394A-2	US-09-620-461-13	US-09-910-174B-13	US-09-620-461-8	US-09-910-174B-8	US-09-303-040-6	US-09-651-200-18	US-09-620-461-10	US-09-910-174B-10	US-09-667-135-36	US-09-910-174B-32	US-09-620-461-17	US-09-910-174B-17	US-09-651-200-25	US-09-620-461-19	
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GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CAN
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-404-879A-392
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309; Conserv
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                                                                  LYNVTINNTYSCMIENDIAKATGDIKVTESEIKRRSHLQLLNSKASLCVSSFFAISWALL
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Pred. No. 1.3e-153;
Mismatches 0;
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PLSPYLMLK 309

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GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

APPLICANT: Algate, Paul A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.462C2

CURRENT APPLICATION NUMBER: US/09/404,879A

CURRENT FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 393

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 393

LENGTH: 282
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Best Local Similarity
Matches 282; Conserv
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Patent No. 6468546
                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version SEQ ID NO 24
                                                                               TYPE: PRT
ORGANISM: Homo sapiens
-09-910-174B-24
   Matches
                                     Query Match
                                                                                                                                                                                             APPLICANT: Coyle, Anthony J.

APPLICANT: Fraser, Christopher C.

APPLICANT: Manning, Stephen
TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
TITLE OF INVENTION: Family and Uses Thereof
FILE REFERENCE: 35800/236924
CURRENT FAPLICATION NUMBER: US/09/910,174B
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 09/620,461
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 32
COMMENT OF SEQ ID NOS: 32
COMMENT PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 32
                                                                                                                                           LENGTH: 316
Local Similarity nes 74; Conserv
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ilarity 28.5%;
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Score 247; DB 4; Length 316; Pred. No. 5.3e-17; i6; Mismatches 106; Indels
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Sequence 4, Application Patent No. 6429303 GENERAL INFORMATION: APPLICANT: Green et al

US/09651200

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RESULT 4
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-620-461-24
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APPLICANT: Coyle, Anthony J.
APPLICANT: Fraser, Christopher C.
APPLICANT: Manning, Stephen
TITLE OF INVENTION: B7-H2 Molecules, No. 66:
TITLE OF INVENTION: Family and Uses Thereof
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Best Local Simi
Matches 74;
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SEQ ID NO 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 5800-149
CURRENT APPLICATION NUMBER: US/09/620,461
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 29
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GNASLRLQRVRVADEGSTICF-VSIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTV 161
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                                                                                                                                                                                                        TITCSSYRGYPEAEVFW--ODGOGVPLTGNVTTS-OMANEOGLEDVHSVLRVVLGANGTY 218
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17-DEC-1998;
23-JUN-1999;
24-SEP-1999;
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                                                                                                                                             17-DEC-1999;
                                                                                                                                                                                               22-JUN-2000
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SXXCCCCCCCCXXXX PFFXXXXXXX
 Query Match
Best Local :
                                                                                   The present invention describes an isolated polypeptide comprising an immunogenic portion of an ovarian carcinoma protein (or its variants). Ovarian carcinoma proteins, and polynucleotides encoding them, have cytostatic activity and can be used in gene therapy and vaccines. Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human ovarian carcinoma polynucleotides and proteins used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                      Immunogenic portion of an ovarian carcinoma protein and the nucleic encoding it, useful for the diagnosis, prevention and treatment of cancer, preferably ovarian cancer.
                                                       Sequence
                                                                                                                                                                                                                                                                        Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                     2000-431589/37.
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                                                                                                                                                                                                                                                                        2; Page 207; 299pp;
                                                       282 AA;
 90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                      Algate
                                                                                                                                                                                                                                                                    English.
Score 1431; DB 3;
Pred. No. 2.2e-117;
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                                                                            WASQVDQGANFSEVSNTSFELNSENVTMKVVSVLYNVTINNTYSCMIENDIAKATGDIKV
                                                                                                                     QLTDAGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAPRWFPQPTVV
                                                                                                                                       QLTDAGTYKCY1ITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAPRWFPQPTVV
               TESEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK
                                                           WASQVDQGANFSEVSNTSFELNSENVTMKVVSVLYNVTINNTYSCMIENDIAKATGDIKV
                                                                                                                                                                                DIKLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNV
                                                                                                                                                                                                            DIKLSDIVIQMLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNV
TESEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK
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282
                             309
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Matches

282;

Conservative

0

Length 282; Indels

Similarity

AAU29132 standard; protein; B

AAU29132;

18-DEC-2001 (first entry)

Human PRO polypeptide sequence #109

RESULT 7
AAU29132
ID AAU2
XX
AC AAU2
AC AAU2
AC AAU2
DT 18-C
XX
DB Huma
XX
PRO
KW DOG;
KW dog;
KW bloc
KW adre
XX
W DO Adre
XX
W DO Adre
XX
W DO Adre
XX
XX
EN WO20
PN WO20
PN 20-S
XX
XX
PF 28-F PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; she dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpi blood; chondrocyte cell; cell proliferation; cell differentiation; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic di

Homo sapiens.

20-SEP-2001

28-FEB-2001; 2001WO-US006520

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Query Match Best Local Sim Matches 282;

Local Similarity

Conservative

0

o ~:

0;

Gaps

0

147 60

120

240 267 180 207 100.0%; 90.9%;

Score 1431; DB 4; 1 Pred. No. 2.2e-117; Mismatches

Length 282; Indels

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29-MAR-2000;

30-MAR-2000;

04-APR-2000;

11-APR-2000;

11-APR-2000;

11-APR-2000;

11-APR-2000;

11-APR-2000;

11-APR-2000;

18-APR-2000;

25-APR-2000;

25-APR-2000;

25-APR-2000;

25-APR-2000;

25-APR-2000;

25-APR-2000;

25-APR-2000;

25-MAY-2000;

30-MAY-2000;

30-MAY-2000;

22-MAY-2000;

22-MAY-2000;

22-AUG-2000;

24-AUG-2000;

24-AUG-2000;

24-AUG-2000;

21-DEC-2000;

21-DEC-2000;
2000WO-US005601.
2000WS-0187202P.
2000US-0189328P.
2000US-0191007P.
2000US-0191007P.
2000US-0191007P.
2000US-0191007P.
2000US-0191007P.
2000US-0191007P.
2000US-0191008-0193032P.
2000US-0193032P.
2000US-0194647P.
2000US-0194647P.
2000US-0194647P.
2000US-0194647P.
2000US-01946820P.
2000US-0196820P.
2000US-0198585P.
2000US-0201516P.
2000US-0201516P.
2000WO-US014941.
2000WO-US014941.
2000WO-US015264.
2000WO-US015264.
2000WO-US030952.
2000WO-US033956.
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GENENTECH INC

Ä, P, Chen J Smith V, v, Watanabe Desnoyers L, Goddard A, Goatanabe CK, Wood WI, Zhang Godowski PJ, ang Z; Gurney AL,

N-PSDB; 2001-602746/68. DB; AAS46033.

Novel nucleic acids encoding PRO polypeptides, used to opresence of tumors, such as prostate and breast tumors, screen for modulators of the compounds. diagnose the and ťο

Claim 11; Fig 218; 774pp; English.

Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention. The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a manmal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breact in mammalian breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic a can be used for genetic analysis of individuals with genetic disord disorders acids

Sequence 282 AA.

Eighty four nucleic acids encoding PRO polypeptides, useful in mol biology, including use as hybridization probes, and in chromosome gene mapping.

molecular

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RESULT 8
AAB87555
ID AAB8
XX
XX
ID AAB8
XX
ID Huma
XX
ID Huma
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ID Huma
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30-MAR-2000;
25-APR-2000;
22-MAY-2000;
05-JUN-2000;
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15-SEP-1999;
07-DEC-1999;
09-DEC-1999;
11-JAN-2000;
18-FEB-2000;
18-FEB-2000;
22-FEB-2000;
01-MAR-2000;
03-MAR-2000;
                                                                                                                                                                                   Eaton DL,
Grimaldi
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)B; AAF92087.
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2000WG-US004341.
2000WG-US004342.
2000WG-US0045601.
2000WG-US005601.
2000WG-0187202P.
2000WG-0191007P.
2000WG-019397P.
2000WG-019397P.
2000WG-019397P.
2000WG-0209832P.
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                                                                                                                                                                                   Gurney
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99US-0169495P.
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Watanabe
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Sequence

309

AA

Similarity

Length

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Best Local S
Matches 309
                                                                                                                                                                 22-FEB-2000;
10-MAR-2000;
07-APR-2000;
15-MAY-2000;
The present invention relates to human breast tumour protein coding sequences (see AAH55479-AAH55513, AAH55517-AAH55679 and AAH55682-AAH55762). The breast tumour protein DNA sequences may be used in ti
                                          Example 3;
                                                                                                                                                                                                                                                                                          Homo
                                                                                            N-PSDB;
                                                                                                                                                                                                         30-NOV-1999;
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                                                                                                                          Dillon
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                                                                                                                                                                                                                                                                                                              antigen;
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                                                                                                                                                                                                                                                                                                                        Cytostatic;
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DB; AAH55681.
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                                                           tumor polypeptides and the prevention, diagnosis and
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                                         Page 191-192;
                                                                                                                                                                99US-00451651.

2000US-00510662.

2000US-00523586.

2000US-00545068.

2000US-00571025.
                                                                                                                         Day CH,
                                                                                                                                                                                                                                                                                                                       human;
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                                                                                                                                                                                                                                                                                                                                                                                                       protein; 309
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                                        221pp; English.
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the

Polypeptides comprising an immunogenic portion of an ovarian carcinoma protein or its variants, useful for stimulating an immune response in patient and treating ovarian cancer.

useful

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ID ABP3
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AC ABP3
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Best Local S
Matches 309
                                                                                                                                                                                                                                                       17-JUL-2000;
10-AUG-2000;
20-SEP-2000;
04-APR-2001;
18-JUN-2001;
                                                                                                                                                Mitcham ,
Reed SG,
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                                                                                    WPI; 2002-164781/21.
N-PSDB; ABN72971.
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Mismatches 0;
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Copyright GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

OM protein protein search, using sw model

May 11, 2004, 16:00:15; Search time 59 Seconds (without alignments) (without alignments)
1479.783 Million cell updates/sec

Title: US-09-827-271-392 1574

Perfect score:

Sequence: 1 HASAHASGRQRQLHSASTQI...SSFFAISWALLPLSPYLMLK 3.09

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

1586107 segs,

282547505 residues

Searched:

1586107

Total number of hits satisfying chosen parameters:

Minimum . BE seq length: 2000000000 length:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1 AAB12556

AAB12556 standard; protein; 309 Ā

AAB12556;

07-NOV-2000 (first entry)

Human ovarian carcinoma antigen O8E protein SEQ ID NO:392.

Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis; tumour antigen; identification; cytostatic; gene therapy; vaccine.

Homo sapiens.

WO200036107-A2.

22-JUN-2000.

17-DEC-1998; 17-DEC-1998; 23-JUN-1999; 17-DEC-1999; 98US-00215681. 98US-00216003. 99US-00338933. 99US-00404879. 99WO-US030270.

(CORI-) CORIXA CORP.

24-SEP-1999;

Mitcham ĴĽ, King GE, Algate PA, Frudakis TN;

WPI; 2000-431589/37.

Immunogenic portion of an ovarian carcinoma protein and the nucleic encoding it, useful for the diagnosis, prevention and treatment of cancer, preferably ovarian cancer. acid

Example 2; Page 205-206; 299pp; English.

The present invention describes an isolated polypeptide comprising an immunogenic portion of an ovarian carcinoma protein (or its variants). Ovarian carcinoma proteins, and polypucleotides encoding them, have cytostatic activity and can be used in gene therapy and vaccines. Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. AAA99691 to AAA70077 and AAB12552 to AAB12557 represent human ovarian carcinoma polynucleotides and proteins used in the exemplification of the present invention

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RESULT 4
ADAO8545
ID ADAO
XX
AC ADAC
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DB Huma
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Matches 309;
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                (MITC/)
(KING/)
(ALGA/)
(FLIN/)
(FLIN/)
(RETT/)
(FANG/)
(REED/)
                                                                                                                                                  18-JUN-2001; 2001US-00884441.
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KING G E.

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VEDVICK T S.
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Pred. No. 6.7e-130;
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Membrane-bound pharmaceutical; Membrane-bound 05-APR-2000 AAY66719; AAY66719

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Best Local Similarity
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No. 6.7e-130;
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22-FEB-2000;
10-MAR-2000;
07-APR-2000;
15-MAY-2000;
                                                     Dillon
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                                                                                                                                                             29-NOV-2000;
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                                                         WASQVDQGANESE
                                                                                   WASQVDQGANFSEVSNTSFELNSENVTMKVVSVLYNVTINNTYSCMIENDIAKATGDIKV
                                                                                                                                   QLTDAGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAPRWFPQPTVV
                                                                                                                                                                                         DIKLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKUV
                                                                                                                                                                                                                                MASLGQILFWSIISIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEP
                                                                                                                                                                                                                                                                                                                                                  282 AA;
                                                                                                               QLTDAGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAPRWFPQPTVV
                                                                                                                                                                       DIKLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASJRLKNV
TESEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 190;
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                          from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis and treatment of breast cancer.
                                                                                                                                                                                                                                                                                                      90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221pp; English.
                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                      Score 1431;
Pred. No. 2.
                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                      .2e-117;
                                                                                                                                                                                                                                                                                                                   DB 4;
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                                                                                                                                                                                                                                                                                                                  Length 282;
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                                                        KSCMIENDIAKATGDIKV
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RESULT 10
AAB65242
ID AAB65
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AC AAB65
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XX
Human
XX
Homo
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                             20-JUL-1999;
26-JUL-1999;
28-JUL-1999;
17-AUG-1999;
15-SEP-1999;
15-SEP-1999;
08-OCT-1999;
30-NOV-1999;
                                                                                                                                                                                                                                                                                                      02-JUN-1999;
23-JUN-1999;
07-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secreted and transmembrane protein; PRO; cytostatic; cancer; chromosomal mapping; gene mapping; tissue typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UNQ659) protein sequence SEQ ID
                         99US-0145698P
99US-0146222P
99US-0149396P
99WO-US021090
99WO-US021547
99US-0158663P
99WO-US028313
                                                                                                                                                                                                                                                                         99US-0141037P.
99US-0143048P.
99US-0144758P.
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cell

AAE20311

AAE20311 standard; protein;

282

Human B7-H8

protein

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Matches
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20-DEC-1999;
05-JAN-2000;
06-JAN-2000;
11-FEB-2000;
11-FEB-2000;
22-FEB-2000;
24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention
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02-MAR-2000;
15-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Ea
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard
Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-032160/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invent
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                               TESEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK
                                                                                                             WASQVDQGANFSEVSNTSFELNSEN
                                                                                                                                              WASQVDQGANFSEVSNTSFELNSENVTMKVVSVLYNVTINNTYSCMIENDIAKATGDIKV 267
                                                                                                                                                                                                                  QLTDAGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAPRWFPQPTVV
                                                                                                                                                                                                                                                              QLTDAGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAPRWFPQPTVV
                                                                                                                                                                                                                                                                                                                               DIKLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNV
                                                                                                                                                                                                                                                                                                                                                                 DIKLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                            MASLGQILFWSIISIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEP
TESETKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK
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2000WO-US000219.

2000WO-US000376.

2000WO-US003565.

2000WO-US004341.

2000WO-US004414.

2000WO-US004914.

2000WO-US005004.

2000WO-US005004.

2000WO-US005004.

2000WO-US0050841.

2000WO-US0050884.

2000WO-US007377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 282;
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  282
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Wood WI;
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Wood
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RESULT 11

The present invention relates to novel human B7-like polypeptides and CC polynucleotides encoding such proteins. Sequences of the invention are used for preventing, treating or ameliorating a medical condition in a manual lan subject. The polynucleotides and polypeptides are administered to subjects having a disorder related to B-7 Like polypeptides, such as CC inappropriate or excessive inflammation which can lead to tissue damage or even death, where the inflammation is brought about by the activation of certain cells in the body e.g. T cells and may involve disorders CC related to immune system. The nucleic acids, proteins, antibodies, agonists and antagonists of the invention are useful in the diagnosis, CC treatment and prevention of cancer (e.g. cancers of the adrenal gland, CC bone, bone marrow, breast, gastrointestinal tract, liver, urogenital or lammon, bone marrow, breast, gastrointestinal tract, liver, urogenital or CC disease, multiple sclerosis, rheumatoid arthritis, ulcerative colitis), CC disease, multiple sclerosis, rheumatoid arthritis, ulcerative colitis), CC cardiovascular disorders (e.g., myocardial ischaemlas), nervous system CC (e.g., cryptorchism, Paget's disease), gastrointestinal disorders (e.g., diabetes mellitus, Grave's disease), reproductive system disorders (e.g., cryptorchism, Paget's disease), gastrointestinal disorders (e.g., hepatitis, hepatitis, bacterial, fungal and epilepsy) and infectious diseases such as viral, bacterial, fungal and parasitic WPI; 200 N-PSDB; Addison's disease; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; allergy; cancer; rheumatoid arthritis; cardiovascular disorder; nervous system disorder; myocardial ischaemia; ulcerative colitis; reproductive system disorder; Alzheimer's disease; Parkinson's disease; endocrine disorder; hepatitis; Isolated nucleic acids encoding human B7-like polypeptides, useful diagnosis and treatment of e.g. inflammation, cancer, immune disord such as Addison's disease, and cardiovascular disorders such as diabetes mellitus; Grave's disease; Paget's disease; liver disorder; gastrointestinal disorder; irritable bowel syndrome; cerebral anoxia; dysphagia; hepatomegaly; neurological disease; infectious disease; epilepsy; gene therapy; B7-H8 protein; chromosome 1. myocardial ischemias. 30-JUN-2000; 2000US-0215135P 14-AUG-2000; 2000US-0225266P Key Example 1; Fig 1; 493pp; English. (HUMA-) WO200202587-A1 Peptide Addison's Human; 2002-257198/30. DB; AAD32519. sapiens. B7-like HUMAN ź Z. 2001WO-US020917 GENOME SCI INC protein; inflammation; tissue damage; 1. .24 /label=_Signal_peptide Location/Qualifiers "Mature B7-H8 protein" immune disorder;

disorders

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RESULT 12
ABG96445
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Best Local Similarity
Matches 282; Conserv
                                                                                                                               19-SEP-2001;
26-SEP-2001;
26-SEP-2001;
                                                                                                                                                                                                                                                                                                                                           Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus brain herniation; inflammation; encephalitis; testicular disorder; nontuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm; historder; ischaemic heart disease; atherosclerosis; neoplasm;
                                                                                                                                                                                                                          14-MAR-2002; 2002WO-US007826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG96445 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 282
                                                                                                                                                                                                14-MAR-2001;
                                                                                                                                                                                                                                                    19-SEP-2002
                                                                                                                                                                                                                                                                              WO200271928-A2
                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infections. Sequences of the invention are also used in gene therapy. present sequence is human B7-H8 protein. B7-H8 gene is located on
                                                 Meyers
                                                                                                                                                                     14-MAR-2001;
10-AUG-2001;
           2002-723277/78
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                                                 RE,
                                                                                        MILLENNIUM
                                  JE, Gannavarapu M, Hoersch S, Kamat
KE, Morrisey MP, Olandt PJ, Sen A,
Lu K, Schmandt RE, Zhao X, Glatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MASLGQILFWSIISIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WASQVDQGANFSEVSNTSFELNSENVTMKVVSVLYNVTINNTYSCMIENDIAKATGDIKV
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                                                                                                               ; 2001US-0276025P.
; 2001US-0276026P.
; 2001US-0311732P.
; 2001US-0323580P.
; 2001US-0324967P.
; 2001US-0325102P.
; 2001US-0325149P.
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                                                                                       INC
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Pred. No. 2.2e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                  Kamatkar S,
en A, Vieby |
Glatt K;
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Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and ы cancer patient.

Disclosure; Page 468-469; 481pp; English

the expression level of a marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as particular use with patients having an enhanced risk of developing convarian cancer (e.g. patients having an familial history of ovarian cancer). The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and control nervous system disorders (e.g. bacterial and confidence (e.g. bacterial of e.g. bacterial or viral meningitis or encephalitis), connective tissue disorders (e.g. nontuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart consective tissue disorders), or heart disorders (e.g. ischaemic heart consecting a composition the progression of ovarian cancer, determining whether ovarian cancer has metastasized or is likely to metastasize, sequence or at risk of developing ovarian cancer. The present amino acid convertion is one of the ovarian cancer markers described in the convertion cancer or at risk of developing ovarian cancer markers described in the convertion. patient is afflicted with ovarian cancer. The method invention relates to a new method for assessing involves comparing whether

Sequence 282 AA;

Similarity

Length 282;

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Best Local S
Matches 282
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                                                                                                                                                                                                                                                                                          282;
                                                                              WASQVDQGANFSEVSNTSFELNSENVTMKVVSVLYNVTINNTYSCMIENDIAKATGDIKV
                                                                                                                                                                         DIKLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNV
                                                                                                                                                                                                    DIKLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNV
                                                                                                                                                                                                                                 MASLGQILFWSIISIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEP
                                                                                                                                                                                                                                                  MASIGQILFWSIISIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEP
                  TESEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK
                                                                                                                 QLTDAGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAPRWFPQPTVV
                                                                                                                                           QLTDAGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAPRWFPQPTVV
TESEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK
                                                        WASQVDQGANFSEVSNTSFELNSENVTMKVVSVLYNVTINNTYSCMIENDIAKATGDIKV
                                                                                                                                                                                                                                                                                        90.9%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                      Score 1431; DB 5;
Pred. No. 2.2e-117;
                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                         0;
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RESULT 13 AAU77766

AAU77766 standard;

protein;

282

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SX BX BX BX BX B

05-JUN-2002

(first

entry)

Tumour

associated

antigenic

target

polypeptide; polypeptide

(TAT)

associated antigenic target

N-PSDB;

ABS76544

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The invention describes an isolated antibody which binds to a tumour-associated antigenic target (TAT) polypeptide. The antibody is useful for: killing a cancer cell (such as a breast, colorectal, lung, ovarian, central nervous system, liver, bladder, pancreatic, cervical, melanoma or leukaemia cell) that expresses a polypeptide with at least 80% identity to the TAT polypeptide sequence; treating a tumour comprising cells that express a polypeptide with at least 80% identity to the TAT polypeptide eith at least 80% identity to the TAT polypeptide sequence; determining the presence of a polypeptide having at least 80% identity to the TAT polypeptide; diagnosing the presence of a tumour in a mammal, and for antibody dependent enzyme mediated prodrug therapy
                                                                                                                                                                                                                                                                                                                             Novel isolated antibody which binds to tumor-associated antigenic target polypeptide useful for killing cancer cells expressing the polypeptide and for treating tumor comprising cells that expresses the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-280928/32.
N-PSDB; ABK11744.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-AUG-2000; 2000WO-US023328
28-FEB-2001; 2001WO-US006520
22-JUN-2001; 2001US-00888257
22-JUN-2001; 2001WO-US020118
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                                                                                                                                                                                                                                                                                     Claim 2;
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Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENENTECH INC.
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/label=
258. .28
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216. .22
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/note= "Tumour associated antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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cal, melanoma or
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RESULT 14
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Best Local Similarity
Matches 282; Conserv
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22-APR-1998;
29-APR-1998;
10-JUN-
11-JUN-
12-JUN-
16-JUN-
17-JUN-
19-JUN-
22-JUN-
24-JUN-
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04-JUN-
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02-JUN-
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SUB6
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-0089514P.
-0089653P.
-0089952P.
-0090246P.
                                                                                                                                                                                                                                                                      defect;
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                                                                      0088824P
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                                                                                                                                                                                                                                                                      osteoarthritis; rheumatoid arthritis
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                                                                                                                                                                                                                                                                                       antirheumatic;
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207 180 267 240 87 60 147

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17-SEP-1998;
27-SEP-1998;
23-SEP-1998;
24-SEP-1998;
24-SEP-1998;
24-SEP-1998;
30-SEP-1998;
06-OCT-1999;
01-SEP-1999;
01-SEP-1999;
01-SEP-1999;
01-SEP-1999;
15-SEP-1999;
15-SEP-199;
15-SEP-1999;
15-SEP-199;
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15-SEP-199
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10-AUG-1998;
17-AUG-1998;
18-AUG-1998;
18-AUG-1998;
26-AUG-1998;
26-AUG-1998;
26-AUG-1998;
01-SEP-1998;
10-SEP-1998;
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10-SEP-1998;
10-SEP-1998;
10-SEP-1998;
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Grimaldi
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16-SEP-1998;
16-SEP-1998;
17-SEP-1998;
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25-JUN-1998;
26-JUN-1998;
                                                                               New isolated secreted and transmembrane PRO polypeptide useful for modulating biological activity of a cell, or for treating sports-rjoint problems, osteoarthritis or rheumatoid arthritis.
 The invention relates polypeptide having 80
                                                                                                                                                    2002-731348/79
DB; ABS74407.
                                                20; Fig 60; 399pp; English.
                                                                                                                                                                                                                                                       GENENTECH
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                                                                                                                                                                                                   Filvaroff
C, Gurney
                                                                                                                                                                                                                                                                                  2000WO-US004341.
2000WO-US004414.
2000WO-US005601.
2000WO-US014042.
2000WO-US015264.
2000WO-US015264.
2000WO-US023522.
2000WO-US023528.
2000WO-US0335873.
2000WO-US03356.
2000WO-US03456.
2001WO-US034566.
2001WO-US034566.
2001WO-US0317443.
2001WO-US017800.
2001WO-US017800.
2001WO-US017800.
2001WO-US017800.
2001WO-US017800.
2001WO-US017800.
2001WO-US017800.
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98US-0100627P.
98US-0100684P.
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RESULT 15
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ID AAU76
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AC AAU76
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AAU76536 standard;

protein;

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CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an extracellular domain of the proteins with their associated signal peptide CC acids encoding the proteins, vectors, host cells, fusion proteins are cardiaged encoding the proteins, vectors, host cells, fusion proteins are considered sendoding the proteins, vectors, host cells, fusion proteins are considered in the specifically bind to the proteins. The proteins are considered in the second peptide designated as E, F, G, H or I (or vice versa) and determining the formation of a N,E, B/F, B/G, C/H or D/I polypeptide conjugate in the sample, where the formation of the conjugate is conjugate in the sample, where the formation of polypeptide, C is a prolloge polypeptide, D is a prolloge polypeptide, C is a prolloge polypeptide, D is a prolloge polypeptide, C is a prolloge polypeptide, D is a prolloge polypeptide, H is a cell suspected of expressing the A, B, C or D polypeptide. H is a cell suspected of expressing the A, B, C or D polypeptide. The sample comprises a cell expressing a polypeptide with a detectable label or is attached to a cell expressing a polypeptide designated as A, B, C or D or E, F, G, C T and the proteins are useful for linking a bioactive molecule is a toxin, a radiolabel or an antibody.

CC The bioactive molecule causes death of the cell. A, B, C or D or E, F, G, H, or I The cell is killed. The proteins are useful for modulating a biological activity of a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H, or I The cell is killed. The proteins are useful for modulating a biological continuity of a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H, or I The cell is killed. The proteins are useful for the treatment of a condition which is responsive to the
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Matches 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful in the treatment of a condition which is its productions, as molecular weight markers for protein electrophoresis purposes, and as therapeutic agents for treating sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. Nucleic acids encoding the proteins are useful as hybridisation probes, in chromosome and gene mapping, in the generation of anti-sense RNA and DNA, for the preparation of the proteins, to generate transgenic or knockout animals which are useful in the development and screening of therapeutic useful reagents, for chromosome identification, and in gene therapy. The antibody is useful as a therapeutic agent, in a diagnostic assay and for affinity purification of the protein from recombinant cell culture natural sources. The present represents a novel secreted or transmembrane protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 282
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Pred. No. 2.2e-117;
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Tumour-associated antigenic target protein,

TAT136.

05-JUN-2002

(first entry)

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The invention relates to an isolated tumour-associated antigenic target polypeptide (TAT) (I), specifically TATI34-TATI38 polypeptides, and the polypucleotides (II) encoding them. (II) is useful for diagnosing the presence of a tumour in a mammal, where the level of expression of (II) is indicative on the presence of tumour in the mammal from which the test sample was obtained. Antibody to (I) is useful for killing a cancer cell, (e.g. breast cancer cell, a colorectal cancer cell, a lung cancer cell, an ovarian cancer cell, a central nervous system (CNS) cancer cell, a liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a
                                                                                                                                                                                                                                                  24-AUG-2000; 2000WO-US023328.

26-SEP-2000; 2000WG-US032678.

01-DEC-2000; 2000WO-US032678.

28-PEB-2001; 2001WO-US006520.

01-MAR-2001; 2001WO-US006666.
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                                                                                                         Claim 12; Fig 8; 121pp;
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                                                                                                                              isolated tumor-associated antigenic target polypeptides which las targets for cancer therapy and diagnosis in mammals.
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1 TD, Zhang
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29. .20
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258. .:
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TESEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK
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ilarity 100.0%;
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Search completed: May Job time : 61 secs time : 11, 2004, 16:21:29

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APPLICANT: Green e
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                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/651,200
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/152383
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/172909
PRIOR FILING DATE: 1999-12-21
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Green et al TITLE OF INVENTION: Polynucleotides Encoding Members of the Human TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and TITLE OF INVENTION: Polypeptides Encoded Thereby FILE REFERENCE: 15966-562 (CURA-62)
                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/:
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 25
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CURRENT APPLICATION NUMBER: US/09/651,200
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/152383
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/172909
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER:
                                                                                    ORGANISM: Homo
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Score
Pred.
246; DB 4;
No. 1.6e-16;
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                 Length 534;
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TYPE: PRT
ORGANISM: Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 15966-562 (CURA-62)
CURRENT APPLICATION NUMBER: US/09/651,200
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/152383
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/172909
PRIOR FILING DATE: 1999-12-21
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PRIOR FILING DATE: 2000-
NUMBER OF SEQ ID NOS: 25
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5. 6429303
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SNTSFELNSENVTMKVVSVLYNVT-INNTYSCMIENDIAK--ATGDIKVT
                                     AAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYRGYPEAEVFW--QDGQGVPLTGN
                                                                        ANLEYKTGA-FSMPEVNVDYN----ASSETLRCEAPRWFFQPTVVWASQVDQGANFSEV
                                                                                                                HSTTEGRD----QGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCF-VSIRDFGS
                                                                                                                                                    HEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRIKNVQLTDAGTYKCYIITSKGKGN 167
                                                                                                                                                                                          VTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSFSPEPGFSLAQLNLIWQLTDTKQLV
                                                                                                                                                                                                                                                                      EVFWQDGQGVPLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPVLQQDAHSS 234
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26.2%; Pred. No. 1.6e-16;
tive 55; Mismatches 111;
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GENERAL INFORMATION:
APPLICANT: Coyle, Anthony J.
APPLICANT: Coyle, Anthony J.
APPLICANT: Fraser, Christopher C.
APPLICANT: Manning, Stephen
TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
TITLE OF INVENTION: Family and Uses Thereof
FILE REFERENCE: 35800/36924
CURRENT APPLICATION NUMBER: US/09/910,174B
CURRENT FILING DATE: 2001-07-20
FRIOR APPLICATION NUMBER: US 09/620,461
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
                                                                                                                                                                                                                                      RESULT 9
US-09-910-174B-28
; Sequence 28, Application US/09910174B
; Patent No. 6630575
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US-09-651-200-2
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PRIOR FILING DATE: 1999-09
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1999-12
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2000-02
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CURRENT APPLICATION NUMBER: US/09/651,
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/152383
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TITLE OF INVENTION: Polynucleotides Encoding Members of the Human
TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
TITLE OF INVENTION: Polypeptides Encoded Thereby
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; LENGTH: 315
; TYPE: PRT
; ORGANISM: Mus
US-09-620-461-28
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; TYPE: PRT
; ORGANISM: Mus r
US-09-910-174B-28
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US-09-620-461-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: 1
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28, Application US/09620461
Patent No. 6635750
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Coyle, Anthony J.
APPLICANT: Fraser, Christopher C.
APPLICANT: Manning, Stephen
TITLE OF INVENTION: B7-H2 Molecules, No. 66
TITLE OF INVENTION: Family and Uses Thereof
FILE REFERENCE: 5800-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/620,461
CURRENT FILING DATE: 2000-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                            179 ---KDGQGVPLTGNVTSQMANERGLFDVHSVLRVVLGANGTVSCLVRNPVLQQDAHGSVT
                                                                                             210 SQVDQGANFSEVSNTSFELNSENVTMKVVSVLYNVT-INNTYSCMIENDIAK--ATGDIK 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 IT 237
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                                                                                                                                                                                                                                                                    95 VIQWIKEGVIGIVHEFKEGKDELSEQDEMERGRTAVFADQVIVGNASIRIKNVQLTDAGT
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                                                                                                                                                                                                                                                                                                           WGGPSVGVCVRTALG-VLCLCLTGAVEVQVSEDPVVALVDTDATLRCSFSPEPGFSLAQL
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Pred. No. 4e-16;
6; Mismatches 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
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Best Local Similarity

26.4%;

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RESULT 12
US-09-620-461-18
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APPLICANT: Fraser, Christopher C.

APPLICANT: Manning, Stephen

TITLE OF INVENTION: B7-H2 Molecules, No. 6630

TITLE OF INVENTION: Family and Uses Thereof

FILE REFERENCE: 35800/236924

CURRENT APPLICATION NUMBER: US/09/910,174B

CURRENT FILING DATE: 2001-07-20

PRIOR APPLICATION NUMBER: US 09/620,461

PRIOR FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-910-174B-18
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LENGTH: 513
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   Query Match
                                                                                                                 SEQ ID NO 18
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Best Local :
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                                                                                                                                                                                                                         APPLICANT: Coyle, Anthony J.
APPLICANT: Fraser, Christopher C.
APPLICANT: Manning, Stephen
TITLE OF INVENTION: B7-H2 Molecules, No. 66
TITLE OF INVENTION: Family and Uses Thereof
                                                                                                                                                   FILE REFERENCE: 5800-149
CURRENT APPLICATION NUMBER: US/09/620,461
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 29
                                                                             LENGTH: 51
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                                                         ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKVV--SVLYNVTINNTYSCMIENDIAKATGDIKVTESEIKRRSHLQLLNSKASLCVSS- 291
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                                                                                                                                   Windows Version 3.0
 14.2%;
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   Score
 223;
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Length 513;
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US-08-724-394A-4
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Patent No.
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                                                                                                                                                  TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587
TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                   FEATURE:
                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                           NAME: Fitts, Renee A. REGISTRATION NUMBER:
                                                                                    STRANDEDNESS:
TOPOLOGY: not
                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
OTHER INFORMATION:
                NAME/KEY: Region LOCATION: 1..540
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                                                                                                                                      LENGTH:
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; LOCATION: (1)...(731)
; OTHER INFORMATION: Xaa =
US-09-910-174B-15
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Best Local Similarity
Matches 62; Consert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Coyle, Anthony J.
APPLICANT: Fraser, Christopher C.
APPLICANT: Manning, Stephen
TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
TITLE OF INVENTION: Framily and Uses Thereof
FILE REPERENCE: 35800/236924
CURRENT APPLICATION NUMBER: US/09/910,174B
CURRENT APPLICATION NUMBER: US/09/910,174B
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 09/620,461
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 32
CORPUNDED: Pastern for Windows Version 4.0
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Best Local :
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SIADPFIQ 241
                                                                 D--SKGENIPAVEG---PVNVYGVGLYAVPPPVIMTGTSGGGVSCIITNSLLGLEKTASI
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                                    KVTESEIK 273
                                                                                                       SQVDQGANFSEVSNTSFELNSENVTMKVV--SVLYNVTINNTYSCMIENDI--AKATGDI
                                                                                                                                                                             GTYKCYIITSKGKGNANLEYKTGAFSMPEVNVD---YNASSETLRCEAPRWFPQPTVVWA 209
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Pred. No. 1.4e-13;
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; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(731)
; OTHER INFORMATION: Xaa = Any Amino Acid
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 15
LENGTH: 731
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Fraser, Christopher C.
APPLICANT: Manning, Stephen
TITLE OF INVENTION: Pamily and Uses Thereof
FILE REFERENCE: 5800-149
CURRENT APPLICATION NUMBER: US/09/620,461
CURRENT FILING DATE: 2000-07-20
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                                                                        179 D--SKGENIPAVEG--
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234 SIADPFÍQ
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1 Similarity 25.0%; Pred. No. 3.6e-13;
62; Conservative 49. Mirmat-
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D39371	A31923	A45803	A57843	S01998	JC7780	I54766	T30805	I48697	I48696	T43290	T20992	JE0099	I49503	JC4211	IJXLNL
Ig V-region-like B	amalgam protein pr	B-cell-restricted	sodium channel bet	contactin precurso	coxsackie- and ade	B-lymphocyte activ	duttl protein - mo	protein-tyrosine k	protein-tyrosine k	hemicentin precurs	hypothetical prote	neural cell adhesi	B-lymphocyte activ	neural adhesion pr	neural cell adhesi

ALIGNMENTS

apical glycopro

RESULT 1 A37821

butyrophilin precursor - human
C; Species: Homo sapiens (man)
C; Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change :
C; Accession: S70587
R; Taylor, M.R.; Peterson, J.A.; Ceriani, R.L.; Couto, J.R.
Biochim. Biophys. Acta 1306, 1-4, 1996
A; Title: Cloning and sequence analysis of human butyrophilin rev.
A; Reference number: S70587; MUID:96201696; PMID:8611614
A; Accession: S70587
A; Status: preliminary
A; Molecule type: mRNA butyrophilin - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 05-Nov-1999
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 # RESULT S70587 γQ B A;Accession: A37821
A;Status: preliminary 5 멍 멂 Š δ A;Cross-references: GB:M35 C;Keywords: transmembrane A; Molecule type: mRNA A; Residues: 1-526 < JAC> 멍 A; Reference number: Cross-references: GB:M35551; NID:g1763685; PIDN:AAB39766.1; PID:g162773 Query Match N Local 102 162 193 135 253 MIENDIAKATGDIKVT 42 75 IGEDGILSCTFEPDIKLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQ 134 l Similarity 49; Conserv LRCEAPRWFPQPTVVWASQVDQGANFSEVSNTSFELNSENVTMKVVSVLYNVTINNTYSC IAEGSVAVRIQEVKASDDGEYRCFFRQDENYEEAIVHLKVAALGSDPHISMKVQESGEIQ 161 VIVGNASLRLKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAF-SMPEVNVDYNASSE-T CIRNLLLGQEKDVEVS VGEDAELPCRLSPNVSAKGMELRWFREKVSPAVFVSREGQEQEGEEMAEYRGRVSLVEDH LECTSVGWYPEPQVQW--RTHRGEEFPSMSESRNPDEEGLFTVRASVIIRDSSMKNV-SC Conservative A37821; MUID:90354441; PMID:2387867 13.9%; protein 234 268 48; Score 219.5; DB 2 Pred. No. 4.5e-09; 8; Mismatches 94 DB 2; Length 526; Indels reveals 21-Jul-2000 <u>ن</u> מ Gaps potential 192 101 218 4.

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R;Rowen, L.; Mahairas, G.; submitted to the EMBL Data A;Description: Sequence of A;Reference number: Z16543 A;Accession: T09058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             butyrophilin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C;Accession: S65133
R;Ishii, T:; Aoki, N.; Noda, A.; Adachi, T.; Nakamura, R.; Matsuda, T.
Biochim. Biophys. Acta 1245, 285-292, 1995
A;Title: Carboxy-terminal cytoplasmic domain of mouse butyrophilin specifical A;Reference number: S65133; MUID:96125722; PMID:8541302
                                                                                                 RESULT 4

T09058

T09058

N;Alternate names: butyrophilin-like protein
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
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A; Residues: 1-487 < ISH>
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A;Cross-references: EMBL:U39576; NID:g1326082; PIDN:AAC50489.1; PID:g1326083
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Best Local S
Matches 44
                                                                                           Accession: T09058
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44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   CEAPRWFPQPTVVWASQVDQGANFSEVSNT--SFELNSENVTMKVVSVLYNVTINNTYSC
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                                                      Qin, S.;
Library,
                                  the mouse major histocompatibility locus class III region.
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Pred. No. 1.9e-05;
1; Mismatches 92;
                                                   Ahearn, M.E.; Dankers, C.; Lasky, October 1997
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                                                                      S.; Loretz,
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997
C;Accession: I46690
R;Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-391 <ROW>
A;Cross-references: EMBL:AF030001,
A;Note: BAC 29N7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Cloning and sequencing of the rabbit gene encoding A;Reference number: I46689; MUID:95369849; PMID:7642234 A;Accession: I46690
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146690
CD80 precursor -
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                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-299 < ISO>
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A; Note: butyrophilin-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 VIVGNASLRLKNVOLTDAGTYKCYIITSKGKGNANLEYKTGAF-SMPEVNV-DYNASSET
                                                                                                                                                                                                                                                                                                       40
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                                                                                                                                                                                                      66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 GEDGILSCTFEPDIKLSDI-VIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQ
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LSVSQIFPWSKPKQEPPIDQLP-
                               IKVTE----SEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYLML
                                                                 LAW---MEDGEELNAV-NTTVDQDLDTELYSVSSELDFNVTNNHSIVCLIK-
                                                                                               VVWASQVDQGANFSEVSNTSFELNSENVTMKVVSVL-YNVTINNTYSCMIENDIAKATGD
                                                                                                                                    C-VVQKNENGSFRREHLTSVTLSIRADFPVPSITDIGHPDPNV--KRIRCSASGGFPEPR
                                                                                                                                                                   CYIITSKGKGNANLEYKTGA--
                                                                                                                                                                                                      QKDQQMVLSII----SGQVEVWPE---YKNRT--FPD--IINNLSLMILALRLSDKGTYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261
                                                                                                                                                                                                                                                                                                                                      Score 163.5; DB 2;
Pred. No. 4.1e-05;
7; Mismatches 89;
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Pred. No. 2.4e-05;
5; Mismatches 82
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Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001
A; Title: Identification of an alternatively spliced variant of human CD86 mRNA.
A; Reference number: JC7604; MUID:21092744; PMID:11162656
A; Molecule type: mRNA
A; Residues: 1-275 < MAG>
C; Comment: This CD86 variant expressed by June 2001
C; Comment: This CD86 variant expressed by June 2001
C; Comment: This CD86 variant expressed by June 2001
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C; Comment: This CD86 variant expressed by June 2001
C; C
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A;Cross-references: EMBL:AL023516;
A;Experimental source: clone cB12
C;Genetics:
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A;Accession: T28138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig V-region-like B-G antigen, isoform 2 - chicken C; Species: Gallus gallus (chicken)
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
C; Accession: T28138
C; Matchan, J.; Beck, S.
submitted to the EMBL Data Library, May 1998
submitted to the EMBL Data Library, May 1998
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C;Superfamily: B-lymphocyte restricted
C;Keywords: immune response
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A; Map position:
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CD86 spliced variant CD86
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                                                               63
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                                                      SITVTTVASAGNIGEDGILSCTFEP--DIKLSDIVIQWLKEGVLGLVHEFKEGKDELSEQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKTRLLSSPFSIGTNTMEREESEQTKKREKIHIPERSDEAQRVFKSSKTSSCDKS
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cring and analysis of the chicken
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23.7%;
-VGQDVVLRCQLSPCKDAWSSD--IRWIQHRTSGFVHHYQNGED--LEQ
                                                                                                                                                  9.6%; Score 151; DB 2;
21.7%; Pred. No. 0.00044;
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6; Mismatches
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Pred. No. 0.00024;
4; Mismatches 99
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A;Reference number: A55717; MUID:95130110; PMID:7829100
A;Accession: A55717
A;Molecule type: DNA
A;Residues: 1-247 < DAU>
A;Cross-references: GB:L29498
A;Cross-references: GB:L29498
A;Cham-Dinh, D.; Mattei, M.G.; Nussbaum, J.L.; Roussel, G.;
Proc. Natl. Acad. Sci. U.S.A. 90, 7990-7994, 1993
A;Title: Myelin/oligodendrocyte glycoprotein is a member of A;Reference number: A47712; MUID:93376728; PMID:8367453
A;Accession: C47712
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                                                                                                                                                                                                                                           myelin/oligodendrocyte glycoprotein precursor - C;Species: Mus musculus (house mouse) C;Date: 23-Mar-1995 #sequence revision 23-Mar-19 C;Accession: A55717; C47712 R;Daubas, P.; Pham-Dinh, D.; Dautigny, A. Genomics 23, 36-41, 1994 A;Title: Structure and polymorphism of the mouse A;Title: Structure and polymorphism of the mouse
 A; Molecule type: mRNA
A; Residues: 30-95, 'E', 97-247
A; Cross-references: GB:L2094;
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A; Introns: 34/1
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A; Residues: 1-340 < MIL>
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A;Accession: T28137
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3',97-247 <PHA>
GB:L20942; NID:g399588;
                                                                                                                                                                                                                           and polymorphism of the A55717; MUID:95130110;
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ce: clone cB12
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32.4%; Pred
32.4%; 22;
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C; Superfamily: E
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A48754
B7-2 antigen - human
N;Alternate names: B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999; C;Accession: A48754; S39055
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                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GDB:433597;
A;Map position: 3q13.3-3q21
C;Superfamily: B7-2 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Azuma, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.I
Nature 366, 76-79, 1993
A;Title: B70 antigen is a second ligand for CTLA-4 and CD28
A;Reference number: S39055; MUID:94050123; PMID:7694153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:L25259; NID:g416368; PIDN:AAA58389.1; PID:g416369
A;Note: it is uncertain whether Met-1 or Met-7 is the initiator
A;Azuma, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Lanier, L.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 262, 909-911, 1993
A;Title: Cloning of B7-2: a CTLA-4 counter-receptor that A;Reference number: A48754; MUID:94053735; PMID:7694363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A48754; S39055
R;Freeman, G.J.; Gribben, J.G.; Boussiotis, V.A.; Ng, J.W.; Restivo Jr., V.
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A; Residues: 7-329 < AZU>
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A; Residues: 1-329 < FRE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: GB:U04343;
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3; Mismatches
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Pred. No. 0.00035;
3; Mismatches 66;
                                                                                                                                                                                                                                                                         Score 147.5;
Pred. No. 0.0
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                                                                                                                                                                                                                                                                                                            DB 1;
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R;Pham-Dinh, D.; Mattei, M.G.; Nussbaum, J.L.; Roussel, G.; Pontarott Proc. Natl. Acad. Sci. U.S.A. 90, 7990-7994, 1993
A;Title: Myelin/oligodendrocyte glycoprotein is a member of a subset A;Reference number: A47712; MUID:93376728; PMID:8367453
A;Accession: B47712
A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                   myelin/oligodendrocyte glycoprotein - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jan-1994 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C;Accession: B47712
C;Accession: B47712
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B47712
A;Molecule type: mRNA
A;Residues: 1-218 <PHA>
A;Experimental source: brain
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C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997
C;Accession: 146691
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C;Superfamily: B7-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
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Pred. No. 0.00078;
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Mismatches
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sequence

extracted

from

NCBI

backbone

(NCBIP:137804)

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C;Genetics:
A;Gene: MOG
C;Function:
A;Description: may be involved in lipid interaction; may be involved in cell-cell commun A;Description: may be involved in lipid interaction; may be involved in cell-cell commun C;Keywords: glycoprotein; myelin; transmembrane protein #status predicted <MAT>
F;1-218/Product: myelin/oligodendrocyte glycoprotein #status predicted <MAT>
F;122-150/Domain: transmembrane #status predicted <TM1>
F;175-200/Domain: transmembrane #status predicted <TM2>
F;31/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig V-region-like B-G antigen 11/4 precursor - chicken (;Species: Gallus gallus (chicken) C;Species: Gallus gallus (chicken) C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 23-Mar-1993 C;Accession: C39371 C;Accession: C39371 R;Miller, M.M.; Goto, R.; Young, S.; Chirivella, J.; Hawke, D.; Miyada, C.G. Proc. Natl. Acad. Sci. U.S.A. 88, 4377-4381, 1991 Proc. Natl. Acad. Sci. U.S.A. 88, 4377-4381, 1991 A;Title: Immunoglobulin variable-region-like domains of diverse sequence within the A;Reference number: A39371; MUID:91239571; PMID:1903541
Ig V-region-like B-G antigen 14/8 precursor - chicken C;Species: Gallus gallus (chicken) C;Date: 20-Mar-1992 #text_cha C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_cha C;Accession: A39371; B39371 C;Accession: A39371; B39371 R;Miller, M.M.; Goto, R.; Young, S.; Chirivella, J.; Hawke, Proc. Natl. Acad. Sci. U.S.A. 88, 4377-4381, 1991 A;Title: Immunoglobulin variable-region-like domains of dive
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A; Residues: 1-372 <MIL>
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                                                                                                                                                                                                                                                NVKLNN-----IAAKLAQQTKELEKQHSQFHRHFQRMDLSAVNQK 302
                                                                                                                                                                                                                                                                                         NVTINNTYSCMIENDIAKATGDIKVTESEIKR---RSHLQLLNSK
                                                                                                                                                                                                                                                                                                                                                                                PRWFPQPTVVWASQVDQGANFSEVSNTSFELNSENVTMKV-------
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Pred. No. 0.0005;
4; Mismatches 47
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                                                                                         20-Mar-1992 #text_change
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myelin/oligodendrocyte glycoprotein precursor - human C;Species: Homo sapiens (man)
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change C;Accession: S58394; S78430; S78431; I56513
R;Hilton, A.A.; Slavin, A.J.; Hilton, D.J.; Bernard, C.C.A.
J. Neurochem. 65, 309-318, 1995
A;Title: Characterization of cDNA and genomic clones encoding hu A;Reference number: S58394; MUID:95310943; PMID:7790876
A;Accession: S58394
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C;Functi
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A;Accession: A39371
A;Status: preliminary
A;Molecule type: mRNA
                A;Description: may be involved in lipid interaction; may be involved in C;Keywords: alternative splicing; glycoprotein; myelin; transmembrane F;1-29/Domain: signal sequence #status predicted <SIG>F;30-247/Product: myelin/oligodendrocyte glycoprotein #status predicte F;351-179/Domain: transmembrane #status predicted <TM1>F;504-229/Domain: transmembrane #status predicted <TM2>F;204-229/Domain: transmembrane #status predicted <TM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:X74511; NID:g984146; PIDN:CAA52617.1; PID:g984147 R;Pham-Dinh, D.; Allinquant, B.; Ruberg, M.; Della Gaspera, B.; Nussbaum J. Neurochem. 63, 2353-2356, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-197, 'GKFRHV'
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A; Accession: S78430
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A; Residues: 1-247 < HIL>
                                                                                                                                                                                                                                                                                                             A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Characterization and expression of the cDNA coding A; Reference number: I56513; MUID:95054056; PMID:7964757
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A; Residues: 1-247 < HID>
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A;Experimental source: adult medulla
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A;Residues: 1-385,387-398
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                                                                                                                                                                                                                                                                                                                                                                                         A;Residues:
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1rences: GB:S73472; NID:g688175;
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Match

Score

144;

DB

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Length

γQ	28	28 MASLGQILFWSIISIIIIAGAIALIIGFGISGRHSITVTTVASAGNIGED 78
Дb	ц	MASLSRPSCLCSFLLLLLLQVSSSYAGQFRVIGPRHPIRALVGDE 48
Qy	79	79 GILSCTFERDIKLSDIVIQWLKEGVLGLYHEFKEGKDELSEQDEMFRGRTAVFADQVIVG 138
DЪ	49	49 VELPCRISPGKNATGMEVGWYRPPFSRVVHLYRNGKDQDGDQAPEYRGRTELLKDAIGEG 108
9	139	139 NASLRLKNYQLTDAGTYKÇYIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAP 198
Db	109	109 KVTLRIRNVRFSDEGGFTCFFRDHSYQBEAAMBLCVEDP 147
γQ	199	RWFPQPTVVWASQVDQGANFSEVSNTSFELNSENVTMKVVSV-LYNVTINNTYSCM 253
Дb	148	148 FYWVSPGVL

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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrat:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_phage:*
11: sp_rodent:*
12: sp_virus:*
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13: sp_vertebrate
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Q9h6b2 homo sapien
Q7tph5 mus musculu
Q7tsp5 mus musculu
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Q7tsp3 mus musculu
Q7zy30 xenopus lae
Q8avv1 xenopus lae
Q8avv1 homo sapien
Q8nc34 homo sapien
Q8nc34 homo sapien
Q8ncb6 homo sapien
Q9nwq6 homo
Q9um44 homo
Q9hcy1 homo
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sapien
sapien
sapien
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4.5	44	43	42										32				28		26				22	21			18	17
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ALIGNMENTS

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RESULT 1
Q7Z7D3
ID Q7Z7D3; PRELIMINARY; PRT; 282 AA.
AC Q7Z7D3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Best Local S
Matches 282
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Sica G.L., Choi I.-H., Zhu G., Tamada K., Wang S.-D., Ta
Chapoval A.I., Flies D.B., Bajorath J., Chen L.;
"Immune inhibition by human B7-H4.";
Submitted (App.-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY280972; AAP37283.1; -.

SEQUENCE 282 AA; 30878 MW; 1C9C565A9242E78C CRC64;
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Mammalia; Eutheria;
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RESULT
Q7TPHS
ID Q7
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AC Q7
DT 01
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Best Local
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01-MAR-2001 (TrEMBLrel. 16, Created
01-MAR-2001 (TrEMBLrel. 16, Last se
01-OCT-2003 (TrEMBLrel. 25, Last an
Hypothetical protein FLJ22418.
Homo sapiens (Human).
                                                                                                                         Q7TPH5;
01-OCT-2003
01-OCT-2003
01-OCT-2003
                                                                                                        B7S1.
                                                     Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Kawabata A., Hikiji T., Kobatake N., Inagaki H., 1
Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi
Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human CDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ data
EMBL; AK026071; BAB15349.1; -.
                                                                                                                                                                                                Q7TPH5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50835; IG_LIKE; 2. Hypothetical protein. SEQUENCE 282 AA; 30893 MW;
    SEQUENCE
                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
SMART; SM00409; IG; 1.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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    N.A.
                                              Chordata;
Rodentia;
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Pred. No. 3.1e
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Sciurognathi;
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annotation update)
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                                                                       Euteleostomi;
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                                                   Murinae;
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Shibahara T.,
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Q7TSP5;
Q1-OCT-2003
01-OCT-2003
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Sica G.L., Choi I.-H., Zhu G., Tamada K., Wang S.-D., Te Chapoval A.I., Flies D.B., Bajorath J., Chen L.;
"Immune inhibition by mouse B7-H4.";
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY280973; AAP37284.1; -.
SEQUENCE 283 AA; 30875 MW; 7E2F174618578519 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Immune costimulatory protein B7-H4.
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EMBL; AY322147; AAP88965.1; -.
SEQUENCE 283 AA; 30847 MW;
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Mammalia; Eutheria;
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Prasad D.V., Richards S., Mai X.M.
"B7S1, a novel B7 family member th
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                                                           OLTDAGTYKCYIITSKGKGNANLEYKTGAFSMÞEVNVDYNASSETLRCEAÞRWFÞQÞTVV
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                WASQVDQGANFSEVSNTSFELNSENVTMKVVSVLYNVTINNTYSCMIENDIAKATGDIKV
                                                                                                     DIKLNGIVIQWLKEGIKGLVHEFKEGKDDLSQQHEMFRGRTAVFADQVVVGNASLRLKNV
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Conservative
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Rodentia;
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                                                                                                                                                                                                                      Score 1257.5;
Pred. No. 1.5e
13; Mismatches
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Pred. No. 6.9e
13; Mismatches
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Q8K091
D7 Q9
AC Q8
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Q7ZY30
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ID Q7ZY30
ID Q7ZY30
ID Q7
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EMBL; BC032925; AAH32925.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig-like.
InterPro; IPR003598; Ig-c2.
Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00409; IGc2; 1.
PROSITE; PS50835; IG LIKE; 2.
Hypothetical protein; Immunoglobulin do; SEQUENCE 283 AA; 30801 MW; 7E581741
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Q8K091;
Q1-OCT-2002 (TrEMBLrel. 22, Created)
Q1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
Q1-OCT-2002 (TrEMBLrel. 25, Last annotation update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to hypothetical protein FLJ22418.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Murida(
                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                       Hypothetical protein (Fragment).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata,
                                Amphibia; Batrachia; Anura;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                         Q7ZY30;
                                                                                                                                                                                                                                                                                                                                                                                 Q7ZY30
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                                                                Mesobatrachia;
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                                                                                                           Vertebrata;
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thi; Muridae; Murinae; Mus
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                                                                                                    Euteleostomi;
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                                                                    Pipidae;
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Matches 105
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Submitted (JAN-2003) to the EMB
EMBL; BC044000; AAH44000.1; -.
InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; IG-like.
SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
PROSITE; PS50835; IG_LIKE; 2.
                                                                                             Klein S., Strausberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ EMBL; BC041253; AAH41253.1; -.
InterPro; IPR007110; Ig-like.
Pfam; PF00047; ig; 2.
PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                01-MAR 2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence up
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Similar to hypothetical protein FLJ2241B.
Xenopus laevis (African clawed frog)
Eukaryota, Metazoa; Chordata; Craniata; Vert
Amphibia, Batrachia; Anura; Mesobatrachia; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Embryo;
                                                                                                                                                                                                       Amphibia; Batrachia; Anura; Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                 SEQUENCE
                                                                                           Hypothetical
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VWASQVDQGANFSEVSNTSFELNSENVTMKVVSVLYNVTINNTYSCMIENDIAKATGDIK
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                                                                                                                                                                                                                                                                                                                                                                          VTESEIKRRSHLQLLNS
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                                                                                al protein.
275 AA; 2
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                                        Conservative
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                                                                                 29751 MW;
                                                 28.5%;
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to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                           283
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Pred. No. 1.2e
50; Mismatches
                                     Score 448; DB 13;
Pred. No. 1.8e-28;
7; Mismatches 98;
                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D937490D361B1B34 CRC64;
                                                                                 5FD1B8FB6BC3A40B
                                                                                                                                                                                                                                                                                                    275
                                                                                                                                                                                                                           Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
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                                        Indels
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Best Local S
Matches 74
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MEDLINE=21163383; PubMed=11224528;
Chapoval A.I., Ni J., Lau J.S., Wilcox R.A.,
Chapoval A.I., Ni J., Wilcox R.A.,
Chapoval A.I., Ni J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Costimulatory molecule.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9BXR1;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 2.
PROSITE; PS50835; IG_LIKE; 2.
SEQUENCE 316 AA; 33791 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF302102; AAK15438.1; -.
GO; GO:0008283; P:cell proliferation;
GO; GO:0006955; P:immune response; NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             production.";
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InterPro; IPR007110; Ig-like.
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                                                                 SCMIENDIAK -- ATGDIKVT
                                                                                                                                                                                                                                                                      GNASLRLQRVRVADEGSFTCF-VSIRDFGSAAVSLQVAAFYSKPSMTLEPNKDLRPGDTV
                                                                                                                                                                                                                                                                                                                                                                                                                TLCCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQD---
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SCLVRNPVLQQDAHGSVTIT
                                                                                                                                TITCSSYRGYPEAEVFW--QDGQGVPLTGNVTTS-QMANEQGLFDVHSVLRVVLGANGTY
                                                                                                                                                                                                 TLRCEAPRWEPQPTVVWASQVDQGANFSEVSNTSFELNSENVTMKVVSVLYNVT-INNTY
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28.5%;
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Last annotation update)
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Pred. No. 5.8e-12;
16; Mismatches 106;
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RESULT
Q8NCB6
ID Q8NCB6
ID Q8
AC Q88
AC Q88
AC Q88
AC Q8
OT 01
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DT 01
DT 01
CT 
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ID Q8NC34
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DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 11-0
DT 01-0
DT 11-0
RP SEQU
RA SIZU
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Q8NCB6;
01-OCT-2002 (TrEMBLrel. 22, Created
01-OCT-2002 (TrEMBLrel. 25, Last se
01-OCT-2003 (TrEMBLrel. 25, Last ar
Hypothetical protein FLJ90368.
Homo sapiens (Human).
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SMART; SM00409; IG; 3.

SMART; SM00407; IGc1; 2.

SMART; SM00408; IGc2; 3.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 3.

Hypothetical protein; Immunoglo SEQUENCE 388 AA; 41768 MW;
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Q8NC34;
01-OCT-2002
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugi Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Sait Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasai Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; "NEDO human cDNA sequencing project."; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AK074997; BAC11344.1; -.
                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002
01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                               VTTS-QMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHGSVTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNTSFELNSENVTMKVVSVLYNVT-INNTYSCMIENDIAK--ATGDIKVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITVTTVAS-----AGNIGEDGILSCTF--EPDIKLSDIVIQWLKEGVLGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QIRWEPSPAMASLGQI-----LF--WSIISIIIILAGAIALIIGFGI---SGRHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVFWQDGQGVPLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPVLQQDAHSS
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(TrEMBLrel. 22, Las
(TrEMBLrel. 25, Las
al protein FLJ90516.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rotein; Immunoglobulin AA; 41768 MW; 44A59F
                            Chordata;
Primates;
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Primates;
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                                                                                                                                                                                                           Created)
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Pred. No. 9.4e-
55; Mismatches
                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Catarrhini;
                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                               sequence update)
annotation update)
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annotation
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No. 9.4e-12;
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i; Hominidae; Homo.
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, Saito K.,
;ahari K.,
Sasaki N.,
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N [1]

& SEQUENCE FROM N.A.

RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Suyar.

RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito

RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K

RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki

RA Hattori A., Okumura K., Twayanagi T., Ninomiya K.;

"NEDO human cDNA sequencing project.";

RI Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

DR InterPro; IPR003599; Ig.

InterPro; IPR003599; Ig-like.

InterPro; IPR003598; Ig_c1.

DR InterPro; IPR003598; Ig_c2.

DR InterPro; IPR003598; Ig_c2.

DR InterPro; IPR003596; Ig_v.

"TON047; ig; 4.
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Best Local S
Matches 76
             SEQUENCE FROM N.A.

Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., H
Ota T., Nishikawa T., Wakamatsu A., Nagai T., N
Saito K., Yamamoto J., Wakamatsu A., Nagai T., N
Nagahari K., Sugano S., Isogai T.,
"HRI human cDNA sequencing project.";
"HRI human cDNA sequencing project.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ da
EMBL; AK075549; BAC11692.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003199; Ig.
InterPro; IPR003199; Ig.
                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TREMBLrel. 25, Last annotation updat
Hypothetical protein NT2RP3001861.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 4.

SMART; SM00409; IG; 4.

SMART; SM00407; IGC1; 2.

SMART; SM00408; IGC2; 4.

SMART; SM00406; IGC2; 4.

PROSITE; PS50835; IG LIKE; 4.

Hypothetical protein; Immunoglobulin domain.

SEQUENCE 533 AA; 57179 MW; FC7B3E3A84F56
                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                 Chordata;
Primates;
Ig.
Ig-like.
Ig_c1.
Ig_c2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 246; DB 4; L
Pred. No. 1.5e-11;
5; Mismatches 111;
                                                                                                                                                                               Craniata; Ve Catarrhini;
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                                                                                                                                                                                  Hominidae;
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                                                                   databases
                                                                                                         Hayashi K.,
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, Saito K.,
ahari K.,
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                                                                                                                       Ishii
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  Query Match
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Best I
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                                         MGD; MGI:2143194; 6030411F23Rik.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 1.
PROSITE; PS50835; IG_LIKE; 2.
SEQUENCE 316 AA; 34001 MW; 78/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003596; Ig_v.
Pfam; PR00047; ig; 4.
SMART; SM00409; IG; 4.
SMART; SM00407; IGc1; 2.
SMART; SM00408; IGc2; 4.
SMART; SM00406; IGv; 2.
PROSITE; PS50835; IG_LIKE; 4.
Hypothetical protein; Immunoglo
SEQUENCE 534 AA; 57265 MW;
                                                                                                                                                     "The B7 family member immune responses.";
                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence up
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Similar to B7 homolog 3 (B7-H3).
6030411F23RIK OR AU016588 OR B7H3.
                                                                                                                                                                                                                                                                                                                                                                        Q8VE98;
                                                                                                             EMBL;
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Mammalia; Eutheria;
                                                                                                                                                                                         STRAIN=C57BL/6;
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                           Submitted
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                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
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Local s
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                                                                                                                      Immunol. 0:0-0(2003).
BC019436; AAH19436.1; -.
AY190318; AAP04007.1; -.
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             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYRGYPEAEVFW--QDGQGVPLTGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSFTEGRD----QGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCF-VSIRDFGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITVTTVAS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVEWQDGQGVPLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPVLQQDAHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANLEYKTGA-FSMPEVNVDYN-----ASSETLRCEAPRWFPQPTVVWASQVDQGANFSEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSFSPEPGFSLAQLNLIWQLTDTXQLV
                                                                                                                                                                                                                           (DEC-2001)
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   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n; Immunoglobulin
57265 MW; OFB1A6
           14.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.6%;
                                                                                                                                                                   Bray M., Yoshinaga S.K.;
r B7-H3 preferentially downregulates
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                                                                                                                                                                                                                          the
 46;
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;
Score 235; DB
Pred. No. 5.6e
46; Mismatches
                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
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Pred.
                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -AGNIGEDGILSCTF--EPDIKLSDIVIQWLKEGVLGLV
                                            7BA30B1E67F55827
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                                                                                                                                                                                                                                                                                                                                                   sequence update)
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No. 1
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                                                                                                                                                                                                                                                                                                                                                                                    316
                       DB 11;
             .6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
.5e-11;
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                    Length 316;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           534;
                                                                                                                                                                      Th1-mediated
  18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          456
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Gaps
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RESULT
Q7TPB4
ID TO 01
DT 01
RF B5
RA 81
RP SI
RA 81
RT 11
RT 11
RT SQ SI
                                RESULT
Q9NWQ6
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                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 66
Q9NWQ6;
Q9NWQ6;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003
01-OCT-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B7H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7TPB4;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Suh W.-K., Chung S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q7TPB4
                                                                                                                                                                                                                                                                                                                                                                          lmmune responses.";
lat. Immunol. 0:0-0
                                           14
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B7 family member
                                                                                                                        179
                                                                              236
                                                                                                   266
                                                                                                                                              210
                                                                                                                                                                     120
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AY190319; AAP04008.1; -.
NCE 316 AA; 34074 MW;
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                                                                                                                                                                                                                                                                                                        66;
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                                                                                                                                                                                                                            VIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGT
                                                                                                                      ---KDGQGLPLTGNVTTSQMANERGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHGSV
                                                                                                                                             SQVDQGANFSEVSN
                                                                                                                                                                                     YKCYIITSKGKGNANLEYKTGAFSMPEVNVDYN-----ASSETLRCEAPRWFPQPTVVWA
                                                                                                                                                                                                               NLIWQLTDTKQLVHSFTEGRD---
                                                                                                                                                                                                                                                          WGGPSVGVSMGTALG-VLCLCLTGAVEVQVSEDPVVALVDTDATLRCSFSPEPGFSLRQL
                                                                                                                                                                                                                                                                                WSIISIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTF--EPDIKLSDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D--GQGVPLTGNVTTS-QMANERGLEDVHSVLRVVLGANGTYSCLVRNPVLQQDAHGSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQVDQGANFSEVSNTSFELNSENVTMKVVSVLYNVT-INNTYSCMIENDIAK--ATGDIK 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGT
                                                                                                                                                                   YTCFVSIQDFDSAAVSLQVAAPYSKPSMTLEPNKDLRPGDMVTITCSSYQGYPEAEVFw-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YTCFVSIQDFDSAAVSLQVAAPYSKPSMTLEPNKDLRPGNMVTITCSSYQGYPEAEVFWK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YKCYIITSKGKGNANLEYKTGAFSMPEVNVDYN----ASSETLRCEAPRWFPQPTVVWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                      14.7%;
|llarity 27.2%;
|Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238
(TrEMBLrel.
                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                   268
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rat).
Da; Chordata;
Da; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                               Bray M.,
r B7-H3 pı
 15,
                                                                                                                                          -TSFELNSENVTMKVVSVLYNVT-INNTYSCMIENDIAK--ATGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222
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preferentially
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Last
 Created)
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                                                                                                                                                                                                                                                                                                   Score 232; DB 11;
Pred. No. 9.8e-11;
4; Mismatches 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                   80FB9D68D0A4143B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence update)
annotation update)
                                                                                                                                                                                                              QGSAYANRTALFPDLLVQGNASLRLQRVRVTDEGS
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y downregulates
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; Murinae; Rat
                                                                                                                                                                                                                                                                                                                              316;
                                                                                                                                                                                                                                                                                                                                                                                               Th1-mediated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus
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RESULT
Q9UM44
  DRAGE RANGE OF THE PROPERTY OF
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Best Local S
Matches 61
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A Hirao M., Ohmori Y., Ota T., Suzuki Y., Obayashi M., Nishi
A Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.,
I "NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK000692; BAA91323.1; -.
R InterPro; IPR003599; Ig.
RInterPro; IPR007110; Ig.
R InterPro; IPR007110; Ig-like.
R Pfam; PF00047; ig; 2.
R SMART; SM00409; IG; 1.
R PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein F
Homo sapiens (Human).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pı
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000
01-MAY-2000
01-OCT-2003
                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=99375318; PubMed=10444326;
Mager D.L., Hunter D.G., Schertzer M., Freema
"Endogenous retroviruses provide the primary
for two new human genes (HHLA2 and HHLA3).";
Genomics 59:255-263(1999).
              Strausberg R.;
Submitted (JUL-2002) to the
EMBL; AF126162; AAD48396.1;
EMBL; BC035971; AAH35971.1;
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                           HERV-H LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UM44
                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                      HHLA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9UM44;
                                                                                                         TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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TISSUE=Ileal mucosa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEIQNGNASLFFRRVSLLDEGIYTCYVGTAIQVITNKVVLKVGVFLTPVMKYEKRNTNSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DQVIVGNASLRLKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVDYNASSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRLDEDIILPSSFE---RGSEVVIHWKYQDSY-KVHSYYKGSDHLESQDPRYANRTSLFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNIGEDGILSCTFEEDIKLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSSYECTIENSLLKQT
                                                                                                                                                                                                                                                                                                                                                                                                                                     0 (TrEMBLrel. 13, Created)
0 (TrEMBLrel. 13, Last sequence update)
3 (TrEMBLrel. 25, Last annotation update)
associating protein 2 (HERV-H LTR-associating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TremBLrel. 15, Last (TremBLrel. 25, Last protein FLJ20685.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 (Human)
HHLA2
                                                                                                                                                                                                                                                                                                                                                  Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.3%; Score 225; DB 4;
31.1%; Pred. No. 2.2e-10;
tive 32; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262
                                                               EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; l
Catarrhini; Hominidae;
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InterPro; IPR007110; Ig-like.
Pfam; PF00047; ig; 3.
SMART; SM00409; IG; 2.
PROSITE; PS50835; IG_LIKE; 2.
SEQUENCE 414 AA; 46850 MW; D645383E1562F70E CRC64;
                                                                                                                                                                                                                          157 LICSVLSVYPRPIITW--KMDNTPISENNMEETGSLDSFSINSP-----LNITGS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 LRCEAPRWFPQPTVVWASQVDQGA----NFSEV-SNTSFELNSENVTMKVVSVLYNVT-I 246
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                                                       SUMMARIES
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45	44	43	42	41	40	39	38	37	36	S S	34
106.5	107.5	109.5	109.5	109.5	110	112.5	112.5	112.5	113	113.5	113.5
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CTX2_HUMAN	CD2 HUMAN	NEO1_RAT	CONT_RAT	SHS1 MOUSE	AXO1_CHICK	CONT_MOUSE	CONT HUMAN	OPCM CHICK	LACH_DROME	NEO1_HUMAN	VGR1_RAT
Q96n03	P06729	P97603	Q63198	P97797	P28685	P12960	Q12860	Q98892	Q24372	Q92859	P53767
homo sapien	homo sapien	rattus norv	rattus norv	m protein-t	gallus gall	mus musculu	homo sapien	gallus gall	drosophila	homo sapien	rattus norv

ALIGNMENTS

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SEQUENCE FROM N.A. STRAINH-BOIStein-Friesian; Davey H.W., Ogg S.L., Husaini Y., Snell R.G., Korobko I.V., Mather I.H., Wilkins R.J.; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases. SEQUENCE FROM N.A. TISSUE-Blood; Seyfert HM., Luethen F.; Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases. [4] CARBOHYDRATE-LINKAGE SITES. MEDLINE-95293916; PubMed=7775382; Sato T., Takio K., Kobata A., Greenwalt D.E., Furukawa K.; Sato T., Takio K., Kobata A., Greenwalt D.E., Furukawa K.; Sato T., Takio K., Kobata A., Greenwalt D.E., Furukawa K.; Sato T., Takio K., Kobata A., Greenwalt D.E., Furukawa K.; Sato T., Takio K., Kobata A., Greenwalt D.E., Furukawa K.; "Site-specific glycosylation of bovine butyrophilin."; J. Biochem. 117:147-157(1995). -!- FUNCTION: May function in the secretion of milk-fat droplets. It may act as a specific membrane-associated receptor for the association of cytoplasmic droplets with the apical plasma membrane. -!- SUBUNIT: Seems to associate with xanthine dehydrogenase/oxidase -!- SUBUNIT: Seems to associate with xanthine dehydrogenase/oxidase -!- SUBUNIT: Seems to associate with mammary tissue and secreted in association with the milk-fat-globule membrane during lactation. -!- SIMILARITY: Belongs to the immunoglobulin superfamily. BTN/MOG family. -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains. -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.	F

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Usage

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Matches 48
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Pfam; PF00622; SPRY; 1.
SMART; SM00406; IGV; 1.
SMART; SM00589; PRY; 1.
SMART; SM00449; SPRY; 1.
PROSITE; PS50835; IG_LIKE; 2
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01-NOV-1997
10-OCT-2003
                                                                     Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
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DOMAIN
 MEDLINE=96201696; PubMed=8611614; Taylor M.R., Peterson J.A., Ceria "Cloning and sequence analysis of
                                                                                                   Butyrophilin p
                                SEQUENCE FROM
TISSUE=Breast;
                                                           NCBI_TaxID=9606;
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InterPro; IPR003596; Ig_v.
InterPro; IPR006574; PRY.
InterPro; IPR003877; SPRY_receptor.
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Z93323; CA
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an email to license@isb-sib.ch).
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1. 42, Last an
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                                                                     Chordata;
Primates;
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE 1.

IG-LIKE V-TYPE 2.

N-LINKED (GLCNAC. . .) (CC

N-LINKED (GLCNAC. . .) (HY

Q -> P (IN REF. 3).

E -> D (IN REF. 1).
Ceriani R.L., Couto J.R.; sis of human butyrophilin
                                                                                                           (Butyrophilin
                                                                                                                                                                                                                                                                                                                                                                     Score 215.5; DB 1;
Pred. No. 1.3e-09;
9; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin domain; Signal; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BUTYROPHILIN
                                                                     Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                            A14126802BD19284 CRC64;
                                                                                                                              update)
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                                                                                                                                                                                                                                                                                                                                                                     ..3e-09;
1ев 94;
                                                                                                                                                            B
                                                                                                           subfamily 1 member
                                                                     Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYBRID)
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Query Match
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Matches 49
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InterPro; IPR001870; B302.
InterPro; IPR001870; Ig-1ike.
InterPro; IPR003596; Ig-v.
InterPro; IPR003596; Ig-v.
InterPro; IPR003577; SPRY_receptor.
Pfam; PF00047; ig; 1.
Pfam; PF00622; SPRY; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGV; 1.
SMART; SM00449; SPRY; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
SEQUENCE
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DOMAIN
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Biochim. Biophys. Acta 1306:1-4(1996).

-!- FUNCTION: May function in the secretion of milk-fat droplets.
may act as a specific membrane-associated receptor for the
association of cytoplasmic droplets with the apical plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between
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SUBUNIT: Seems to associate with xanthine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY:
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219 YIQN 222
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                                                                                                                                                                                                              75 IGEDGILSCTFEPDIKLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQ
                                                                                                                                                                                                                                               49;
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                                                                                                                                                                                                                                                               Similarity
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                                                        LECTSVGWYPEPQVQW--RTSKGEKFPSTSE-SRNPDEEGLFTVAASVIIRDTSTKNVSC
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Belongs to the
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iss Institute of Bioi
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Pred. No. 2.6e
37; Mismatches
                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE 1.
IG-LIKE V-TYPE 2.
N-LINKED (GLCNAC. . .) (PO
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EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin domain; Signal; Repeat BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasma
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Bioinformatics
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RESULT 3
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SMART; SM00589; PRY; 1.
SMART; SM00449; SPRY; 1.
PROSITE; PS50835; IG_LIKE;
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Pfam;
                                                                                                                                                           Transmembrane;
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochim. Biophys. Acta 1245:285-292(1995).

-!- FUNCTION: May function in the secretion of milk-fat may act as a specific membrane-associated receptor fassociation of cytoplasmic droplets with the apical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ishii T., Aoki N., Noda A., Adachi T., Nakamura "Carboxy-terminal cytoplasmic domain of mouse k specifically associates with a 150-kDa protein cells and milk fat globule membrane.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ogg S.L., Komaragiri M.V.S., Mather I.H.; "Structural organization and mammary-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Butyrophilin precursor BTN1A1 OR BTN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatithe European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96125722; PubMed=8541302;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 39-487 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      butyrophilin gene.";
Mamm. Genome 7:900-905(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=129; TISSUE=Mammary gland; MEDLINE=97148936; PubMed=8995761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
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15-JUL-1998 (Rel. 36, Last
15-MAR-2004 (Rel. 43, Last
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                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                              InterPro;
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                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       membrane (By similarity).

SUBUNIT: Seems to associate with xanthine dehydrogenase/oxidase.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: Expressed in mammary tissue and secreted in association with the milk-fat-globule membrane during lactation.

DEVELOPMENTAL STAGE: Expression increases during the last half of pregnancy and is maximal during lactation.

STMILARITY: Belongs to the immunoglobulin superfamily. BTN/MCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Contains 2 immunoglobulin-like V-type domains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:103118;
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                                                                                                                                                                                                                                                                                              PF00047; ig; 1. PF00622; SPRY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U67065; AAB51034.1;
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                                                                                                                                                                                                                                                                                                                                      ); IPR001870; B302.

); IPR007110; Ig-like.

); IPR003596; Ig v.

); IPR006574; PRY.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                email to license@isb-sib.ch).
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annotation update)
) (Butyrophilin subfamily 1 member
BUTYROPHILIN.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE 1.

IG-LIKE V-TYPE 2.

N-LINKED (GLCNAC. . .) (PO'
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tions as long as its content
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                                                                                                                                                                                   Immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ., Nakamura R., Matsuda
of mouse butyrophilin
Da protein of mammary ep
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                                                                                                                                                                            domain; Signal;
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01-NOV-1995
01-NOV-1995
10-OCT-2003
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CONFLICT
                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                         use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                    Immunogenetics 42:217-220(1995).

-!- FUNCTION: Involved in the costimulatory signal lymphocytes activation. T cell proliferation are production is induced by the binding of CD28 of
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=B/J X CHBB:HM;
MEDLINE=95369849; PubMed=7642234;
                                                                                                                                                                                                                                                                                                                                         antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                         RABIT
                    or send
                                                                                                                                                                                                     costimulatory molecules
                                                                                                                                                                                                              Isono T., Seto A.;
"Cloning and sequencing of the rabbit
                                                                                                                                                                                                                                                                                                                    Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   lymphocyte
                                                                                                          SUBCELLULAR LOCATION: Type I membrane SIMILARITY: Contains 1 immunoglobulin-SIMILARITY: Contains 1 immunoglobulin-
                                                                                                                                                                                                                                                                                                                                                                                                             RABIT
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                   s requires a license agreement ( an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VIVGNASLRLKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAF-SMPEVNVDYNASSE-T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGSDAELTCGFSPNASSEYMELLWFRQTRSTAVLLYRDGQEQEGQQMTEYRGRATLATAG
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                                                                                                                                                                                                                                                                                                                    cuniculus
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(Rel. 32, Last sequence update)
(Rel. 42, Last annotation updat
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46
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                                                                                                                                                                                                                                                                                                                                                    activation antigen
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423
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Chordata; Craniata; Ve
Lagomorpha; Leporidae;
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                                                                                                           immunoglobulin-like C2-type
immunoglobulin-like V-type c
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D -> DD (IN REF. 2).
V -> F (IN REF. 2).
E -> D (IN REF. 2).
R -> S (IN REF. 2).
V -> E (IN REF. 2).
T -> K (IN REF. 2).
SL -> FF (IN REF. 2).
PRRV -> LAEY (IN REF. 2).
DIPLSPLGEGCTSGDKDT -> C
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Pred. No. 1.1
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                               (See
                                        There are no restrictions ng as its content is in ved. Usage by and for co
                                                                                                                                                                                                                                                                                            Vertebrata; Eu
ae; Oryctolagus
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                                                                                                                                  protein.
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                              http://www.isb-sib.ch/announce/
                                                                                                                                                                                                              encoding
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CTLA-4 to
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                                                                                                            domain.
                                                                                                                       domain
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Best Local S
Matches 73
immunoglobulin |
J. Neurosci. Res
[2]
                                                                                                                                 Q63345;
01-NOV-1997
01-NOV-1997
                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=93085763; PubMed=1453482;
Gardinier M.V., Amiguet P., Linington C.,
"Myelin/oligodendrocyte glycoprotein is a
                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
DOMAIN
                                                                  Rattus norvegicus (Rat)
Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Rod
NCBI_TaxID=10116;
                                                                                                               01-NOV-1997 (Rel. 35, C
01-NOV-1997 (Rel. 35, L
10-OCT-2003 (Rel. 42, L
Myelin-oligodendrocyte
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InterPro; :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [mmunoglobulin domain;
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; IPR007110;
; IPR003599;
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                                                                                                                                                                                                                                                            VVWASQVDQGANFSEVSNTSFELNSENVTMKVVSVL-YNVTINNTYSCMIENDIAKATGD
                                                                                                                                                                                                                                                                            C-VVQKNENGSFRREHLTSVTLSIRADFPVPSITDIGHPDPNV--KRIRCSASGGFPEPR
                                                                                                                                                                                                                                                                                                                                                    LCLLLALAG---
                                                                                                                                                                                                                                                                                                                                                                    ISIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI-KLSDIVIQW
                                                                                                                                                                                                                                                                                            CYIITSKGKGNANLEYKTGA-----FSMPEV----NVDYNASSETLRCEAPRWFPQPT
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          Res.
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               superfamily
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        33:177-187 (1992)
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TG_LIKE;
T-c
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                                                                             Chordata;
Rodentia;
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Ig.
                                                                                                                                                                                                                                                                                                                                                                                              10.4%;
                                                                                                                                                                                                                                                                                                                                                   LHFSSGIS----QVTK----
                                                                                                                        Last sequence update)
Last annotation updat
                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-cell;
                                                                                                               glycoprotein
                                                                                                                                                                                                                                                                                                                -SGQVEVWPE---YKNRT--FPD--IINNLSLMILALRLSDKGTYT
                                                                                                                                                                                                                                                                                                                                                                                                                          WW;
                                                                                                                                                                                                                                                                                                                                                                                       57;
                                                                                                                                                                                                                                                                                                                                                                                      Score 163.5;
Pred. No. 8.3e
57; Mismatches
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N-LINKED
N-LINKED
N-LINKED
N-LINKED
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CYTOPLASMIC (POTENTIAL)
IG-LIKE V-TYPE.
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                                                                           Craniata; Vertebrata;
Sciurognathi; Muridae
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KTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                          6744223E5CC91DE0
                                                                                                               precursor.
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                                                                             Muridae;
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                          member
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                                 J.-M.;
                                                                           Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL)
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Best Loc
Matches
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DISULFID
CARBOHYD
SEQUENCE
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TISSUE=Brain;
MEDLINE=93376728; PubMed=8367453;
Pham-Dinh D., Mattei M.-G., Nussb.
Pontarotti P., Roeckel N., Mather
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Albouz-Abo S., Wilson J.C., Bernard C.C.A., von Itzstein M.;
"A conformational study of the human and rat encephalitogenic
oligodendrocyte glycoprotein peptides 35-55.";
Eur. J. Biochem. 246:59-70(1997).
-!- FUNCTION: Minor component of the myelin sheath. May be inv
completion and/or maintenance of the myelin sheath and in
cell communication.
-!- SUBCULIULAR LOCATION: Integral membrane protein.
-!- SUBCELLULAR LOCATION: Found exclusively in the CNS, where it
                                                                                                                                                                                                                                   SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                          EMBL; M99485; AAA41628.1;
EMBL; L21995; AAF74786.1;
PIR; B47712; B47712
                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collab
between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 histocompatibility complex
                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                      InterPro; IPR007110;
InterPro; IPR003596;
                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                      entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR OF 62-82 MEDLINE=97354172; PubMed=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Myelin/oligodendrocyte glycoprotein is a immunoglobulin superfamily encoded within
                                                                                                                                                                                                                                                           mmunoglobulin
                                                                                                      Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     membranes.
DEVELOPMENTAL STAGE: A
DEVELOPMENTAL DAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY:
CAUTION: DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to
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ACTIVE MYELINATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          localized on
                                                                                                                                                                                                                                                                 PF00047; ig; 1.
I; SM00406; IGv; 1.
ITE; PS50835; IG LIKE;
             85
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                                  ហ
                                                                                39;
                                                                                           Similarity
requires a
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                                  WSLSLPSCLLSLLLLLQLSRSYAGQFR-VIGPG----HPIRAL
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28
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177
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245
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                                                                              Conservative
                                                                                                                                                                                                                                               domain;
                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contains 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the surface of myelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=9210466;
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176
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229
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139
                                                                                                                                                                                                                                                                                                    Ig-like.
Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                      license agreement
                                                                                                                             27881
                                                                                          9.7%;
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                                                                                                                                                                                                                                                        Glycoprotein; Myelin; Transmembrane; Signal.
                                                                                                                             MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoded
                                                                              31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoglobulin-like V-type domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEAK OF EXPRESSION HAS BEEN OBSERVED 15 AND 25, COINCIDENT WITH THE PERIO
                                                                             Score 152; DB
Pred. No. 5.3e
31; Mismatches
                                                                                                                                                                       EXTRACELLULAR POTENTIAL. CYTOPLASMIC (POTENTIAL. EXTRACELLULAR
                                                                                                                            N-LINKED (GLCNAC. . .) (P
C97F8AD60D6A32B4 CRC64;
                                                                                                                                                                                                                      MYELIN-OLIGODENDROCYTE GI
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                    POTENTIAL.
                                                                                                                                                               IG-LIKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoglobulin
                                                      AGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCT
                                                                                                                                                                                                                                                                                                                                                                                    noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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                                                                                         DB 1;
                                                                                                                                                                                                (POTENTIAL)
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a the CNS, where it
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zt K., Lindahl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  superfamily.
                                                                                                   Length 245;
                                                                              Indels
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                                                                                                                                                                                                                                  GLYCOPROTEIN
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                                                                                                                                       (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 gh a collaboration -
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                                  -VGDEAELPCR
                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   involved in cell-
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RESULT 6
MAG MOUSE
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                                                                                                                                                                                                                                                                         STRAIN=BALB/c; TIBBURE-1373175;

MEDILINE=92218912; PubMed=1373175;

Amiguet P., Gardinier M.V., Zanetta J.-P., Matthieu Purification and partial structural and functional of mouse myelin/oligodendrocyte glycoprotein.";

J. Neurochem. 58:1676-1682(1992).

-i- FUNCTION: Minor component of the myelin sheath.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOG MOUSE STANDARD; PKI; 2
Q61885; P70364; Q62003;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Gardinier M.V., Matthieu
"Murine and human MOG are
            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                    "Myelin/oligodendrocyte glycoprotein is a member of immunoglobulin superfamily encoded within the major histocompatibility complex."; proc. Natl. Acad. Sci. U.S.A. 90:7990-7994(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                             -!- DISEASE: Reduced concentrations of MOG are
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 29-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dautigny A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pham-Dinh D., Mattei
Pontarotti P., Roeck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BALB/c;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glycoprotein gene
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"Structure and polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95130110; PubMed=7829100;
Daubas P., Pham-Dinh D., Dautigny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93376728; PubMed=8367453;
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                                                                                                                                                                                                       cell communication.
SUBUNIT: May form homodimers.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Found exclusively in the CNS, where localized on the surface of myelin and oligodendrocyte
                                                                                                      SIMILARITY:
CAUTION: Do
                                                                                                                                                quacking dysmyelinating mutant SIMILARITY: Belongs to the immu
                                                                                                                                                                                                 membranes.
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                                                                                 {\tt ION:} Do not confuse myelin-oligodendrocyte glycoprotein oligodendrocyte-myelin glycoprotein (OMG).
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QNVRFSDEGGYTCFFRDHSYQEEAAVELX 141
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Roeckel N., Mather I.H., Artz
                                                                                                                    Contains
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e highly conserved:
m. 24:234-234(1993)
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                                                                                                                    immunoglobulin-like V-type
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characterization
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Best Local S
Matches 34
                                                                                                                                                          O75144; Q9HD18; Q9NRQ1;
15-JUL-1999 (Rel. 38, Created)
16-OCT-2001 (Rel. 40, Last sequence up:
10-OCT-2003 (Rel. 42, Last annotation:)
ICOS ligand precursor (B7 homolog 2) ((B7-related protein-1) (B7RP-1).
ICOSL OR B7H2 OR B7RP1 OR KIAA0653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L29501;
EMBL; L29499;
EMBL; L29502;
EMBL; U64572;
EMBL; L20942;
           MEDLINE=20477846; PubMed=11023515; Wang S., Zhu G., Chapoval A.I., Dong "Costimulation of T cells by B7-H2,
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EMBL;
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                                                      SEQUENCE FROM N.A
                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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SMART; SM00406; IGv;
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InterPro; IPR003596;
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Catarrhini;
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ATGMEVGWYRSPFSRVVHLYRNGKDQDAEQAPEYRGRTELLKETISEGKVTLRIQNVRFS
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L -> LL (IN REF.
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Dong H., Tamada K.,
-H2, a B7-like molec
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(IN REF. 3)
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(B7-H2)
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                                                                                                                   Vertebrata; Euteleostomi;
                                                                                                     Hominidae;
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molecule
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Chen L.;
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SEQUENCE FROM N.A. (ISOFUKM 1), SEQUENCE FROM N.A. (ISOFUKM 1), SEQUENCE PROM N.A. (ISOFUKM 1), FINANCE S.D., MINER TISSUE=Peripheral blood lymphocytes;

MEDLINE=20465019; PubMed=11007762;

Yoshinaga S.K., Zhang M., Pistillo J., Horan T., Khare S.D., Miner Yoshinaga S.K., Zhang M., Pistillo J., Dai T., Delaney J., Han H., Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H., Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.;

"Characterization of a new human B7-related protein: B7RP-1 is the "Characterization of a new human B7-related protein: B7RP-1 is the
between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U entities requires a license agreement (See htt or send an email to license@isb-sib.ch).
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This SWISS-PROT entry is copyright. It is preceded to the substitute of Bioinformatics and the substitute of Bioinformatics and the rest in the substitute of Bioinformatics and the substitute. There are no rest in the substitute of Bioinformatics and the substitute of Bioinformatics are substituted of Bioinformatics and substitute of Bioinformatics are substituted of Bioinformatics and substitute of Bioinformatics are substituted of Bioinformatics and substituted of Bioinformatics are substituted of Bioinfo
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-i- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR ICOS. ACTS AS A COSTINULATORY SIGNAL FOR T-CELL PROLIFERATION AND CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND DIFFERENTIATION INTO PLASMA CELLS. COULD FLAY AN IMPORTANT ROLE IN MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY COSTIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O., "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."; DNA Res. 5:169-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 2).
Ling V., Dunussi-Joannopolulos
"G150 molecules and uses theref
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Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka
Kotani H., Nomura N., Ohara O.;
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Ling V., Wu P.W.,
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J. Immunol. 164:1653-1657(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Leukocyte;
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ISOId=075144-2; Sequence=VSP 002520;
TISSUE SPECIFICITY: ISOFORM 1 TS WIDELY EXPRESSED (BRAIN, HEART, KIDNEY, LIVER, LUNG, PANCREAS, PLACENTA, SKELETAL MUSCLE, BONE MARROW, COLON, OVARY, PROSTATE, TESTIS, LYMPH NODES, LEUKOCYTES, SPLEEN, THYMUS AND TONSIL), WHILE ISOFORM 2 IS DETECTED ONLY IN LYMPH NODES, LEUKOCYTES AND SPLEEN.

INDUCTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY TREATMENT WITH TUF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND MONOCYTES, WHILE IT IS DECREASED IN DENDRITIC CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 1 immunoglobulin-like SIMILARITY: Contains 1 immunoglobulin-like CAUTION: Ref.4 sequence differs from that s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MONOCYTES, WHILE IT IS DECREASED IN DENDRISHMENTS: Belongs to the immunoglobulin
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molecules and uses therefor.";
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ke C2-type domain
t shown in positio
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CD86 HUMAN STANDARD; PRT; 329 AA. P42081; Q13655; 01-MOV-1995 (Rel. 32, Created) 01-MOV-1995 (Rel. 32, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) T lymphocyte activation antigen CD86 precurso antigen) (CTLA-4 counter-receptor B7.2) (B70)
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SMART; SM00409; IG; 1.
PROSITE; PS50835; IG_L
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InterPro; IPR003599; Ig.
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GHV -> ES
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IG-LIKE V-TYPE.
IG-LIKE C2-TYPE.
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EXTRACELLULAR (POTENTIAL).
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647934E21B55E34A CRC64;
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     EMBL;
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MEDLINE=94348060; PubMed=7520767;
Engel P., Gribben J.G., Freeman G.J., Z
Nadler L.M., Wakasa H., Tedder T.F.;
"The B7-2 (B7-2 costimulatory modes of the control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Freeman G.J., Gribben J.G., Boussiotis V.A., Restivo V.A. Jr., Lombard L.A., Gray G.S., N "Cloning of B7-2: a CTLA-4 counter-receptor cell proliferation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell
J. I
                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activated B lymphocytes is the CD86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95088403; PubMed=7527824;
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Immunogenetics 42:85-89(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Upou (8/) and CD86 (870) provide similar Il proliferation, cytokine production, a Immunol. 154:97-105(1995).
                                                                                                                                                                                                                                                                                                                                                                                    for T lymphocyte proliferation and interleukin 2 production, be binding CD28 or CTLA-4. May play a critical role in the early events of T cell activation and costimulation of naive T cells such as deciding between immunity and anergy that is made by T cells within 24 hours after activation.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: Expressed by activated B lymphocytes and
                                                                                                                                                                                                                                                                                                          SIMILARITY: Contains 1 immunoglobulin-like C2-type domain. SIMILARITY: Contains 1 immunoglobulin-like V-type domain. DATABASE: NAME-PROW; NOTE=CD guide CD86 entry;
                                                                                                                                                                                                                                                                                        DATABASE: NAME=PROW; NOTE=CD guide CD86 entry; www="http://www.ncbi.nlm.nih.gov/prow/cd/cd86.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          od 84:1402-1407(1994).
FUNCTION: Receptor involved in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   er L.L., Somoza C.;
antigen is a second ligand
re 366:76-79(1993).
                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced throusen the Swiss Institute of Bioinformatics and the
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PROSITE; PS00290; IG_MHC; FALSE_NEG.
PROSITE; PS00290; IG_MHC; FALSE_NEG.
              B lymphocyte antigen).
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                                                                                                                                                                                                                                                                                            SEQUENCE
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InterPro; IPR003006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cells within 24 hours after activation.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Contains 1 immunoglobulin-like C2-type.
SIMILARITY: Contains 1 immunoglobulin-like V-type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            runogenetics 44:41/-44010/.

FUNCTION: Receptor involved in the costimulatory signal essent for T lymphocyte proliferation and interleukin 2 production, k binding CD28 or CTLA-4. May play a critical role in the early events of T cell activation and costimulation of naive T cells activation and anergy that is made by '
                          156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I46691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D49842; BAA08642.1; -.
                                                                55
                                                                                                  96
                                                                                                                                       12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM00406; IGv;
                                                                                                                                                                                                                                    Similarity
   KCYIITSKGKG-----NANLEYKTGA-FSMPEVNVDYNA---
                                                          VFWQDQERL-VLYELFLGREKPDNVDPKYIGRTSF--DQ-
                                                                                                                                           TVFVMALLLSGAASLRI
                                                                                                                                                                           SIISIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTF--EPDIKLSDIV
                                                                                                IQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR003596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seto A.;
                                                                                                                                                                                                                                                                                              330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cuniculus (Rabbit).
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Metazoa; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                           23
248
248
269
269
33
150
157
157
135
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213
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                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I46691.
                                                                                                                                                                                                                                                                                              AA;
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                                                                                                                                                                                                                                                                                                                                ; Ig-like.
; Ig_MHC.
; Ig_v.
; 1.
                                                                                                                                                                                                                                    9.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T-cell;
                                                                                                                                                                                                                                                                                              MW,
                                                                                                                                                                                                                  44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                            N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                               Score 147.5; DB 1;
Pred. No. 0.00018;
4; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
CYTOPLASMIC (POTENTIAL)
IG-LIKE V-TYPE.
IG-LIKE C2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B LYMPHOCYTE !
EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                            935CDD65C57E3EE1
                                                                                                                                                                                                                                                                                                              (GLCNAC. . . (GLCNAC. . . )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      There are no restrictions ng as its content is in wed. Usage by and for conventions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIVATION I
                                                                                                                                       QAYFNKTADLPCQFTNSQSRSLSELV
                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                    Length 330;
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-ESWNLQLHNVQIKDKGVY
                                                                                                                                                                                                                                                                                                          (POTENTIAL).
(POTENTIAL).
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RESULT
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                                                                                                                                                                                                      SEQUENCE FROM N.A., AND ALTERNATIVE SPLIC
MEDINE=96115584; PubMed=8666381;
Pham-Dinh D., della Gaspera B., de Rosbo
"Structure of the human myelin/oligodenda
multiple alternative spliced isoforms.";
Genomics 29:345-352(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOG HUMAN STANDARD; PRT; 247 AA Q16653; 000713; 000714; 000715; Q13054; Q13 Q92892; Q92893; Q92894; Q92895; Q93053; Q96 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
              Eur.
                       STRUCTURE BY NMR OF 64-84.

MEDIINE=97354172; PubMed=9210466;

Albouz-Abo S., Wilson J.C., Bernard C.C.A., v
"A conformational study of the human and rat oligodendrocyte glycoprotein peptides 35-55."

Eur. J. Biochem. 246:59-70(1997).
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDIINE=96015053; PubMed=8530032;

Roth M.-P., Malfroy L., Offer C., Sevin J., Enault G
Pontarotti P., Coppin H.;

"The human myelin oligodendrocyte glycoprotein (MOG)
nucleotide sequence and structural characterization.
                                                                                                                                                                                                                                                                                                                                                                                           Nussbaum J.-L., Dautigny A.; "Characterization and expression of the myelin/oligodendrocyte glycoprotein."; J. Neurochem. 63:2353-2356(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oligodendrocyte glycoprotein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND ALTERNATIVE SPI
MEDLINE=95310943; PubMed=7790876;
Hilton A.A., Slavin A.J., Hilton D.J.,
"Characterization of cDNA and genomic of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                             Submitted
                                                                                                                         Griffiths
                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                            Submitted
                                                                                                                                                                        Ballenthin
                                                                                                                                                                                  SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95054056; PubMed=7964757; Pham-Dinh D., Allinguant B., Rube
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myelin-oligodendrocyte glycoprotein
                                                                                                                                                  [6]
                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurochem. 65:309-318(1995).
             FUNCTION: Minor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210
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                                                                                                                                                            n P.A., Gard
(SEP-1996)
                                                                                                             (APR-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Human)
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                                                                                                                                                          A., AND ALTERNATIVE SPLICING
Gardinier M.V.;
996) to the EMBL/GenBank/DDB
                                                                                                                                   (ISOFORMS 1; 5
component of the or maintenance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Primates;
                                                                                                                                                                                                                                                                     AND ALTERNATIVE SPLICING
                                                                                                             5
                                                                                                             the
                                                                                                             EMBL/GenBank/DDBJ
                                                                                                                                                            EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                  1godendrocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 AA
                                                                                                                                   7).
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Q96KU9;
                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA coding
                                                                                                                                                                                                                                                                                                                                                                                                                                          della Gaspera
                                                                                                                                                                                                                                           N.K.,
  myelin
 sheath. May
elin sheath
                                               von Itzstein M.;
L_encephalitogenic
                                                                                                                                                                                                                                                                                                                                           Enault G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rd C.C.A.;
encoding
                                                                                                             databases
                                                                                                                                                            databases
                                                                                                                                                                                                                               Dautigny A.; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q14855; Q92891; Q96KV0; Q99605;
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             May
                                                                                                                                                                                                                                                                                                           gene:
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B
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and
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involved in cell-
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InterPro; trac.

Pfam; PE00047; ig; l.

ProceITE; PS50835; IG J
                                                     Genew; HGNC:7197
MIM; 159465; -.
GO; GO:0007417; J
                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       membranes.
SIMILARITY:
family.
SIMILARITY:
CAUTION: DO
CAUTION: DO
                                                                                             ; X74511; CAA52617.1; -...
; Z18051; CAA88109.1; -...
; U18840; AAC50362.1; -...
; U18798; AAC50876.1; -...
; U18799; AAC50877.1; -...
; U18800; AAB36870.1; -...
; U18801; AAC50879.1; -...
; U18803; AAC50879.1; -...
; U18803; AAC60879.1; -...
; U64564; AAB08089.1; -...
; U64565; AAB08089.1; -...
; U64567; AAB08091.1; -...
; U64569; AAB08091.1; -...
; U64570; AAB08091.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: Found exclusively in the CNS, where localized on the surface of myelin and oligodendrocyte c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell communication.
SUBUNIT: May form homo- or hete subcorms.
SUBCELLULAR LOCATION: Integral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAUTION: Do not confuse myelin-oligodendrocyte with oligodendrocyte-myelin glycoprotein (OMG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=2; Synonyms=Alpha-2;
IsoId=Q16653-2; Sequence=VSP_002543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=6; Synonyms=Beta-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=4; Synonyms=Alpha-4;
IsoId=Q16653-4; Sequence=VSP_002539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=3; Synonyms=Alpha-3;
IsoId=Q16653-3; Sequence=VSP_002542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q16653-6; Sequence=VSP_002543, me=7; Synonyms=Beta-3; IsoId=Q16653-7; Sequence=VSP_002542,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ime=5; Synonyms=Beta-1;
IsoId=Q16653-5; Sequence=VSP_002545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the adult;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q16653-9; Sequence=VSP_002540,
Note=Not functionally active. May be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ime=8; Synonyms=Beta-4;
IsoId=Q16653-8; Sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ime=1; Synonyms=Alpha-1;
IsoId=Q16653-1; Sequence=Displayed;
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                                                                                 HGNC:7197; MOG
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                                       P:central nervous 7110; Ig-like.
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LIKE; 1.
n; Glycoprotein;
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                                                                                             ALT SEQ.
ALT SEQ.
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                                                        system
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 Myelin;
                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                        development;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSP_002541;
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Transmembrane;
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Best Local &
Matches 49
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SEQUENCE
SEQUENCE FROM N.A.

MEDILINE=94065585; PubMed=7504059;
Freeman G.J., Borriello F., Hodes R.J., Reise:
My J.W., Kim J., Goldberg J.M., Hathcock K., 1
Wang S., Gray G.S., Nadler L.M., Sharpe A.H.;
"Murine B7-2, an alternative CTLA4 counter-rea
                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
T lymphocyte activation antigen CD86 precursor (annotation)
antigen) (Early T cell costimulatory molecule-1)
                                                                                                                                                                         CD86
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DOMAIN
TRANSMEM
                                                                                                       CD86
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01-NOV-1995
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                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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SIGNAL
                                                                NCBI_TaxID=10090;
                                                                                             Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                           KVTLRIRNVRFSDEGGFTCFFRDHSYQEEAAME
                                                                                                                                                                                                                                                                            NASLRLKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAP
                                                                                                                                                                                                                                                                                                VELPCRISPGKNATGMEVGWYRPPFSRVVHLYRNGKDQDGDQAPEYRGRTELLKDAIGEG
                                                                                                                                                                                                                                                                                                                  GILSCTFEPDIKLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVG
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                                                                            Rodentia;
                                                                                   Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                               MW;
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Pred. No. 0.00
39; Mismatches
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/FTId=VSP 002544
RNPF -> LFHLEALSG (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPHFLRVPCWKITLFVIVPVLGPLVALIICYNWLHRRLA
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MYELIN-OLIGODENDROCYTE GLYCOPROTEIN.
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V \rightarrow L (IN REF. 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                           Craniata; Vertebrata; : Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTId=VSP
                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTId=VSP
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                                                                                                                                                                                                                                                                                                                                                                                                              -> L (IN REF. 3).
847601FE5997AB0C CRC64;
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                              Reiser H.,
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                     K., Laszlo
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; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isoform
                   Lombard L.A.,
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THE THE THE TWO DOES AND DOES 
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EMBL; U39462; AAC523
EMBL; U39464; AAC523
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EMBL; U39466; AAC523
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DISULFID
DISULFID
CARBOHYD
                                                                                                                      TRANSMEM DOMAIN DOMAIN
                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                             SMART; SM0406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; FALSE
PROSITE; PS00290; IG_MHC; FALSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen C., Gault A., Shen L., Nabavi N., "Molecular cloning and expression of eamolecule-1 and its characterization as J. Immunol. 152:4929-4936(1994).
                                                                                                                                                                                                                                                                                                Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Receptor involved in the costimulatory signal essention for Tymphocyte proliferation and interleukin 2 production, by binding CD28 or CTLA-4. May play a critical role in the early events of T cell activation and costimulation of naive T cells, such as deciding between immunity and anergy that is made by T cells within 24 hours after activation.

SUBCELLULAR LOCATION: Type I membrane protein.

SIBCELCITY: Expressed on activated B cells.

SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;; L25606; AAA79770.1; U39456; AAC52334.1; U39462; AAC52334.1; U39462; AAC52334.1; U39463; AAC52334.1; U39466; AAC52334.1; U39466; AAC52336.1; U39466; AAC52336.1; U39464; AAC52336.1; U39466; AAC52336.1; U39464; AAC52336.1; U39464; AAC52336.1; U39465; AAC52336.1; U39466; AAC52336; AAC52336; U39466; AAC52336; U39466; AAC52336; U39466; AAC52336; U
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T LYMPHOCYTE
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Glycoprotein;
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ate mB7-2 transcripts.
                                                                                             C2-TYPE
                                                                                                                        A-TYPE
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        (GLCNAC.
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                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                         ACTIVATION
                                                                                                                                                                                                           (POTENTIAL)
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BOVIN
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P55803;
01-NOV-1997
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                                                                                                                                                      TISSUE=Brain;
MEDLINE=93382604; PubMed=8371836;
MEDLINE=93382604; PubMed=8371836;
Birling M.C., Roussel G., Nussbaum F., Nussbaum J.-L.;
"Biochemical and immunohistochemical studies with specific studies and immunohistochemical studies with specific studies and immunohistochemical studies with specific stu
                                                                                                                                                                                                                                                                                           "Myelin/oligodendrocyte glycoprotein is a immunoglobulin superfamily encoded within histocompatibility complex."; Proc. Natl. Acad. Sci. U.S.A. 90:7990-7994
                                                                                                                                                                                                                                                                                                                                                                             Pham-Dinh D., Mattei M.-G., Nussba
Pontarotti P., Roeckel N., Mather
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myelin-oligodendrocyte
                                                                                                                                                    glycoprotein.";
                                                                                                                                                                                                                                                              SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                               Dautigny A.;
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93376728; PubMed=8367453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9913;
              cell communication.
SUBUNIT: May form homodimers.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Found exclusively in the CNG
TISSUE SPECIFICITY: Found exclusively and oligodene
                                                                                                 FUNCTION: Minor component of completion and/or maintenance
                                                                                                                      FUNCTION: Minor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELNSENVTMKVVSVLYNVTI---
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                                                                                                                                    18:937-945 (1993)
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35, Last sequence update)
42, Last annotation updat
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Cetartiodactyla; Ruminantia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 143.5;
Pred. No. 0.00
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the myelin sheath a
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minantia; Pecora; Bovoidea;
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                cytoplasmic
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Best Local S
Matches 31
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P13592; P13593;
01-JAN-1990 (Rel
                                                                 Elsom V., Moore S.E., Goridis C., Walsh F.: "Complete sequence and in vitro expression phosphatidylinositol-linked N-CAM isoform i
                                                                                                                                                                                                                                                                                                                                      01-JAN-1990 (Rel. 13, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
Neural cell adhesion molecule 1, 120 kDa isoform
(NCAM-120) (CD56 antigen).
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DOMAIN
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                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
           SEQUENCE OF 491-761
                                                                                                                                 Barton
                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Skeletal mu
                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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PIR; A47712; A47712.
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                                                Development
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Immunoglobulin domain;
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CAUTION: Do
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rPro; 1PR007110; 1
rPro; 1PR003596;
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                                                                                                                             C.H., Dickson G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oligodendrocyte-myelin glycoprotein (OMG).
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                                                                                                                                                                                                                                                         Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
         (ISOFORM N-CAM
                                                                                                          H.J., Rowett L.H.,
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of a tissue-specific
from skeletal muscle.";
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This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentions and the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=87301755; PubMed=2887295; Dickson G., Gower H.J., Barton C.H., Prentice H.M., Elsom V Moore S.E., Cox R.D., Quinn C., Putt W., Walsh F.S.; "Human muscle neural cell adhesion molecule (N-CAM): ident: of a muscle-specific sequence in the extracellular domain. Cell 50:1119-1130(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Alternative splicing and brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=89077552; PubMed=3203385; Gower H.J., Barton C.H., Elsom V. Dickson G., Walsh F.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [3]
SEQUENCE OF 491-655 FROM
SEQUENCE OF 777552; PubMed:
entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Skeletal muscle;
                                                                                                                                                                                         SIMILARITY: Contains 5 immunoglobulin-like C2-type d. SIMILARITY: Contains 2 fibronectin type III domains. DATABASE: NAME=PROW; NOTE=CD guide CD56 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd56.htm".
                                                                                                                                                                                                                                                                                         Name=C; Synonyms=Secreted; IsoId=P13592-1; Sequence=VSP_02587;
                                                                                                                                                                                                                                                                                                                                                                         Name=N-CAM 120;
IsoId=P13592-2;
Name=N-CAM 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurites, etc.
SUBCELLULAR LOCATION:
ALTERNATIVE PRODUCTS:
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FUNCTION: This protein is a cell neuron-neuron adhesion, neurite
                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=3;
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(See http://www.isb-sib.ch/announce, gh a collaboration EMBL outstation -

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MIM; 116930; -.

GO: GO:0016021; C:integral to membrane; TA
GO; GO:0005886; C:plasma membrane; TAS.
InterPro; IPR008957; FN III-like.
InterPro; IPR003961; FN III.
InterPro; IPR003961; FN III.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig-c2.
Pfam; PF00041; fn3; 2.
Pfam; PF00047; ig; 5.
SMART; SM00408; IGc2; 5.
SMART; SM00408; IGc2; 5.
PROSITE; PS50835; IG LIKE; 5.
Immunoglobulin domain; Cell adhesion; Glyc.
Immunoglobulin domain; Cell adhesion; Glyc.
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PIR; S07784; IJHUNG.
Genew; HGNC:7656; NCAM1.
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EMBL; M17409; AAA59912.1; --
EMBL; M22094; AAA59910.1; --
EMBL; M22092; AAA59911.1; --
EMBL; M22091; AAA59911.1; JO
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Best Local &
Matches 64
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P13591; Q15829; Q16180;
01-JAN-1990 (Rel. 13, Created)
15-JUL-1998 (Rel. 36, Last sequence updation of the control of the contro
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE=94356433; PubMed=8075973;

Matter S., Tanio Y., Tachibana I., Hayashi S., Kishimoto T., Kawase : Saito S., Tanio Y., Tachibana I., Hayashi S., Kishimoto T., Kawase : "Complementary DNA sequence encoding the major neural cell adhesion "complecule isoform in a human small cell lung cancer cell line.";

Lung Cancer 10:307-318(1994).
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SEQUENCE OF 491-848 FROM N.A. MEDLINE=87301755; PubMed=2887295; Dickson G., Gower H.J., Barton C
                                                                                                                                                                   MEDLINE=91250739; PubMed=1710251; Lanier L.L., Chang C., Azuma M.,
                                                                                   "Molecular and functional analysis associated neural cell adhesion molor, Immunol. 146:4421-4426(1991).
                                                                                                                                                 Lanier L.L., C
Phillips J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
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entities or send a
                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :- :-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Human muscle neural cell adhesion of a muscle-specific sequence in the Cell 50:1119-1130(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moore S.E.,
                                                                                                                                                                                                                                                                                      SIMILARITY: Contains 5 immunoglobulin-like C2-
SIMILARITY: Contains 2 fibronectin type III do
DATABASE: NAME=PROW; NOTE=CD guide CD56 entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Type I membraLITERNATIVE PRODUCTS:
Event=Alternative splicing; Named
                                                                                                                                                                                                                                                                 WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd56.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P13591-1; Sequence=Displayed;
Name=N-CAM 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurites, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuron-neuron adhesion, neurite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: This protein is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=N-CAM 140;
                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P13592-2; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                            .me=C; Synonyms=Secreted;
IsoId=P13592-1; Sequence=External;
                                                                                    s requires a license agreement (S an email to license@isb-sib.ch).
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molecule (N-CAM)
he extracellular
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                                                                                                       noved. Usage by and for commercial
  (See http://www.isb-sib.ch/announce/
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EMBL; S71824; AAB31836.1; EMBL; U63041; AAB04558.1; EMBL; M17410; AAA59913.1; HSSP; P40189; 1BQU.
Genew; HGNC:7656; NCAM1. DOMAIN
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0; GO:0016021; C:integral to membrar
0; GO:0005886; C:plasma membrane; T;
nterPro; IPR008957; FN_III-like.
nterPro; IPR003961; FN_III.
nterPro; IPR0071110; Ig-like.
nterPro; IPR003598; Ig_c2. 709 730 730 116 212 230 308 440 660 660 660 411 139 223 534 74 442 347 847 847 847 847 847 847 848 splicing adhesion; CYTOPLASMIC
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RESULT 15
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Matches 64
                                                                                                                                                                                                                                                                                        Protein-tyrosine phosphatase non-receptor type substrate 1 precursor (SHP substrate-1) (SHPS-1) (Inhibitory receptor SHPS-1) (Signal-regulatory protein alpha-1) (Sirp-alpha-1) (Sirp-alpha-2) (Sirp-alpha-3) (MYD-1 antigen) (Brain Ig-like molecule with tyrosine-based activation motifs) (Bit) (Macrophage fusion receptor) (p84).

PTPNS1 OR SHPS1 OR SIRP OR MYD1 OR BIT OR MFR.
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                                                                                                                  N-GLYCOSYLATION, A
                                                                                                                                                            Fujioka Y., Kasuga M., "Mouse and human SHPS-localization of genes.
        SEQUENCE FROM N.A.
ARG-107; GLY-109 A
                                                                                   Kharitonenkov
                                                                                             MEDLINE=97215901;
                                                                                                       TISSUE=Placenta;
                                                                                                                                                 Biochem.
                                                                                                                                                                                          MEDLINE=97223399; PubMed=9070220;
Yamao T., Matozaki T., Amano K.,
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                   SHS1_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRILARGEINFKDIQVIVNVPPTIQARQNIVNATANLGQSVTLVCDA-EGFPEPTMSWTK
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                                                     of proteins .";
                                                                                                                                                                                                                                                            Eutheria;
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93360
          AND
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                                                                                                                                                                      SHPS-1: molecular
                                                                                 PubMed=9062191;
Chen Z., Sures
                                                                                                                  (ISOFORM 1), POLYMORPHISM, I
                 (ISOFORM 3), AND
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Primates;
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L -> F (IN REF. 2)
QG -> R (IN REF. 3
MISSING (IN REF. 3)
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); Mismatches
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7; Q8TAL8; C
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                                                                                                                                                 231:61-67 (1997).
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                                                                                                                                                                                            Matsuda
                                                            signalling
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                  VARIANTS ASP-95; LEU-96; ASN-100,
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                                                                                                                            PHOSPHORYLATION
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                                                             tyrosine
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                                                             kinase
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RX MEDILINE=21638749; PubMed=11780052;

RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

RA Dones M., Stavrides G., Almeida J.P., Babbage A.K., Beaguley C.L.,

RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,

RA Basley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Basley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

RA Cligg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

RA Cligg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

RA Cligg S., Cobley V.E., Markland J.A., Fraser A., French L., Garner P.,

RA Cligg S., Cobley V.E., Heath P.D., Ho.S., Holden J.L., Howden P.J.,

RA Humbond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,

RA Huckle E., Hunt A.R., King A., Knights A., Laird G.K., Lawlor S.,

RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

RA Millim S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

RA Millimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

RA Rice C.M., Ross M.T., Scott C.E., Sebra H.K., Shownkeen R., Sims S.,

RA Swain R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

RA Whitehead S.L., Whittaker P., Willy D.L., Williams L., Williams S.A.,

RA Whitehead S.L., Whittaker P., Willy D.L., Williams S.A.,

RA Milliams L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

RA Roders J.;
                                                            MEDLINE-22388257; pubMed-12477932;

XMEDLINE-22388257; pubMed-12477932;

XMEDLINE-223825;

XMEDLINE-22388257; pubMed-12477932;

XMEDLINE-223825;

XMAX., Schaefer L., Max L., Chent N.K.,

XMEDLINE-223825;

XMEDLINE-223825;

XMEDLINE-223825;

XMEDLINE-223825;

XMAX., Schaefer L., Max L., M
human and mouse cDNA sequences. Proc. Natl. Acad. Sci. U.S.A. 9 [7]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THR-52; ARG-54; ALA-57; GLY-109 AND VAL-131. TISSUE=Brain, Kidney, ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20053880;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rs J.;
DNA sequence and comparative
re 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 structure of mouse BIT/S
em. J. 344:667-675(1999).
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ALA-57;
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hi H., Kubota M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISOFORM 1),
(-75; ASP-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H., Kubota M.;
mouse BIT/SHPS-1.";
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bers of the SIRP alpha family of protein tyrosine
proteins in cattle that are expressed on monocyto
of dendritic cells and which mediate binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLY-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Skin;
                         99:16899-16903 (2002)
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LEU-96; ASN-100;
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Bentley D.R., Beck S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome 20.";
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, Bhat N.K.,
, Hsieh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARG-107;
                                                                                                                                                                                                Sanchez
| G.G.,
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J. Immunol. 167:2547-2554(2001).

-I- FUNCTION: Immunoglobulin-like cell surface receptor for CD47. A as docking protein and induces translocation of PTPN6, PTPN11 a other binding partners from the cytosol to the plasma membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gignal
                                                          between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---
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Latour S., Tanaka H., Demeure C., Mateo V
Maliszewski C., Lindberg F.P., Oldenborg
Delespesse G., Sarfati M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stofega M.R., Argetsinger L.S., Wang H., Ullrich A., Carter-Su C., "Negative regulation of growth hormone receptor/JAK2 signaling by signal regulatory protein alpha.";
                                                                                                                                                                                   This SWISS-PROT
between the Swi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD47 and its cognate receptor signal-regulator protein-alpha: down-regulation of IL-12 responsiveness and inhibition of dendritic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION BY JAK2, AND INTERACTIONS MEDLINE=20428742; PubMed=10842184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                multi-protein complexes in macrophages.";
Curr. Biol. 9:927-930(1999).
                                      entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Timms J.F., Swanson K.D., Marie-Cardine A., Raab M., Rudd C.E., Schraven B., Neel B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION, AND INTERACTIONS WITH FYB; SCAP2 AND PTK2B. MEDLINE=99401000; PubMed=10469599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Bidirectional negative regulation of human T and dendritic cells by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "SHPS-1 is a scaffold for assembling distinct adhesion-regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol.
send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: No experimental confirmation available in brain.
TISSUE SPECIFICITY: Ubiquitous. Highly expressed in brain.
Detected on myeloid cells, but not T cells. Detected at lower levels in heart, placenta, lung, testis, ovary, colon, liver, levels in heart, placenta, spleen, kidney, skeletal muscle an
                                                                                                                                                                                                                                                                             stimulation with EGF, growth hormone, insulin and PDGF. Dephosphorylated by PTPN11.
SIMILARITY: Contains 2 immunoglobulin-like C1-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Binds PTPN11 when tyrosine-phosphorylated, except in macrophages, where it primarily binds PTPN6. Binds GRB2 in vit Binds FGR (By similarity). Binds JAK2 irrespective of its phosphorylation status and forms a stable complex. Binds SCAP1 and/or SCAP2. The resulting complex recruits FYB. Binds PTK2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of phagocytosis, mast cell activation and dendritic cell activation. CD47 binding prevents maturation of immature dendritic cells and inhibits cytokine production by mature dendritic cells.
                                                                                                                                                                                                                                                                                                                                                                                                   PTM: N-glycosylated.
PTM: Phosphorylated on tyrosine residues in stimulation with EGF, growth hormone, insuli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Type I membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adhesion, growth factors or insulin. Mediates negative regulation of phagocytosis, mast cell activation and dendritic cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity). Involved in the negative regulation of receptor tyrosine kinase-coupled cellular responses induced by cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Supports adhesion of cerebellar neurons, neurite outgrowth and glial cell attachment. May play a key role in intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         signaling during synaptogenesis and in synaptic function (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note=No experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P78324-3; Sequence=VSP_007029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P78324-2; Sequence=VSP_007030;
Note=No experimental confirmation available;
an email
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275;28222-28229(2000).
                                                                                                                            entry is copyright. It is produced through a collaboration iss Institute of Bioinformatics and the EMBL outstation oinformatics Institute. There are no restrictions on its
to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mateo V., Rubio M., Brown E.J., denborg A., Ullrich A.,
                               (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WITH PTPN11 AND JAK2
                                                                 Usage
                                                                                             its content
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Best Local
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EMBL; Y11047; CAA71944 1; ALT INIT.
EMBL; AB023430; BAA87929.1; -.
EMBL; AL034562; CAB38874.1; -.
EMBL; AL034562; CAB38874.1; -.
EMBL; AL049634; CAB46662.1; ALT_SEQ.
EMBL; AL107335; CAC12723.1; -.
EMBL; BC033092; AAH26692.1; -.
EMBL; BC033092; AAH33092.1; -.
EMBL; BC038510; AAH38510.1; -.
                                                                                                                                                                                                                                                                                                                         EMBL; BC03851,
PIR; JC5287; JC5287.
Genew; HGNC:9662; PT
MIM; 602461; -.
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EMBL;
EMBL;
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Y10375;
Y11047;
  210
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                                                                                                                                                                                                                                          23 EPS-PAMASIGQILFWSIISIIIILAGAIALIIGFGISGRHSITVTTVASAGNI--GEDG
                                                                                                                                                                                                                                                                       64;
                                                                                                                                                                                                                                                                                                                                                   HGNC:9662; PTPNS1
                                                                                                                                                                                                                                                                                    Similarity
 STAKVVLTREDVHSQVICEVAHVT---
                                                                                                                                FADQVIVGNASLRLKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVDYNASS
                                                     PVVSGPAARATPQHTVSFTCESHGFSPRDITLKWFKNGNELSDFQTNVDPVGESVSYSIH
                                                                                                                                                                                       ILSCTFEPDIKLSDIVIQWLKEG--VLGLVHEFKEGK-----DELSEQDEMFRGRTAV 130
                                                                                                                                                                                                                EPAGPAPGRIGPLI-----CLLLAASCA---WSGVAGEEELQVIQPDKSVSVAAGESA 51
                          SNTSFELNSENVTMKVVSVLYNVTINNTYSCMIENDIAKATGDIKVT
                                                                              ETLRCEAPRWFPQPTVVWASQ-
                                                                                                        -----DFSISISNITPADAGTYYC---VKFRKGSPDTEFKSGAGT--ELSVRAKPSA
                                                                                                                                                              ILHCTVTSLIPVGP--IQWFRGAGPARELIYNQKEGHFPRVTTVSESTKRENM------
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAA12974.1;
                                                                                                                                                                                                                                                                                 8.5%;
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                                                                                                                                                                                                                                                                                 Score 134.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                     Mismatches
-LQGDPLRGTANLSET
                                                                                                                                                                                                                                                                                  .0033;
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                                                                             ---VDQGANFSEV
248
                           268
                                                                                                                                                                                                                                                                                               503;
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                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                 190
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12

Job time : 18 secs Search completed: May 11, 2004, 16:21:58

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Result
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being primand is derived by analysis of the total score distribution.
                                                                seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications AA:*

1: -/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10RW_PUB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10RW_PUB.pep:*

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18: /cgn2_6/ptodata/2/pubpaa/US10RW_PUB.pep:*
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            US-09-827-271-392
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                                             6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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      US-09-778-320-209
US-09-984-441-392
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US-10-198-053-392
US-09-778-320-208
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1824.854 Million cell updates/sec
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Sequence 209, Appx

Sequence 309, App

Sequence 392, App

Sequence 392, App

Sequence 392, App

Sequence 209, App

Sequence 209, App

Sequence 208, App

Sequence 208, Appl

Sequence 8, Appli

Sequence 291, App

Sequence 291, App
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9-990-437-29	-866-60-	-09-989-726-29	-09-990-711-29	9-990-562-29	-09-990-438-29	-09-997-666-29	S-09-997-428-29	S-09-993-667-29	-09-997-653-29	S-09-989-734-29	-09-993-687-	-09-990-436-	09-989-730-	-09-991-181-	-09-990-444-	-09-989-735-	-09-989-2931	-09-915-7891	9-896-738-	-09-992-598-2	09-989-721-2	-09-990-456-2	-993-604-2	-09-991-163-2	-09-990-442-2	9-991-073-2	-09-989-732-2	9-884-4	US-09-989-731-291
equence 291	Ø	equence 291	equence 291	equence 291	e 291	equence 291	equence 291	equence 291	ce 291	Sequence 291	equence 291,	equence 291,	e 291,	equence 291,	equence 291,	equence 291,	e 291,	equence 5,	equence 2,	e 291	equence 291	291	291	291	equence 291	equence 291	equence 291	equenc	91

ALIGNMENTS

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-778-320-209
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US-09-778-320-209
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Patent No. Usav.
GENERAL INFORMATION:
GENERAL DISTONMENT C.
Craig H.
                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 210121.491C5
CURRENT APPLICATION NUMBER: US/09/778,320
CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ 10 NOS: 301
SOFTWARE: FASTSEQ for Windows Version 3.
SEQ ID NO 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 209, Application Patent No. US20010034052A1
                                                                                                                                                                               Matches
                                                                                                                                                                                                              Query Match
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APPLICANT:
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APPLICANT:
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APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                          y Match 100.0%; s
Local Similarity 100.0%; I
hes 309; Conservative 0;
 121
                                    61
                                                                      13
                                                                                                                           1 HASAHASGRORQLHSASTQIRWEPSPAMASLGQILFWSIISIIIILAGAIALIIGFGISG
DEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAFSMP 180
                                                          RHSITVTTVASAGNIGEDGILSCTFEPDIKLSDIVIQWLKEGVLGLVHEFKEGKDELSBQ 120
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Mitcham, Jennifer
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Pred. No. 6.5e-138;
Mismatches 0;
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APPLICANT: Day, Craig H.

APPLICANT: Day, Craig H.

APPLICANT: Houghton, Raymond L.

APPLICANT: Houghton, Raymond L.

APPLICANT: Houghton, Jennifer

APPLICANT: Mang, Tongtong

APPLICANT: Mang, Tongtong

APPLICANT: Mang, Tongtong

APPLICANT: Harlocker, Susan L.

ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEE

TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER

FILE REFERENCE: 210121.491C6

CURRENT APPLICATION NUMBER: US/09/910,689

CURRENT APPLICATION NUMBER: US/09/910,689

CURRENT FILING DATE: 2001-07-20

NUMBER OF SEQ ID NOS: 307

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 209

LENGTH: 309

TYPE: PRT

ORGANISM: Homo sapiens

US-09-910-689-209
RESULT 3
US-09-884-441-392
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Best Local S
Matches 309
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Sequence 392, Application US/09884441

Patent No. US20020119158A1

GENERAL INFORMATION:

APPLICANT: Algate, Paul A.

APPLICANT: Carter, Darrick

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C7

CURRENT APPLICATION NUMBER: US/09/884,441

CURRENT FILLING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 489

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 392

LENGTH: 309

TYPE: PRT

ORGANISM: Homo sapiens

US-09-884-441-392
                                                    APPLICANT: King, Gordon E.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

APPLICANT: Fling, Steven P.

APPLICANT: Fling, Steven P.

APPLICANT: Fanger, Marc W.

APPLICANT: Fanger, Gary Richard

APPLICANT: Reed, Steven G.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Hill, Paul

APPLICANT: Albone, Barl

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C8

CURRENT APPLICATION NUMBER: US/09/907,969

CURRENT FILING DATE: 2001-07-17

NUMBER OF SEQ ID NOS: 596
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US-09-907-969-392
SOFTWARE: FastSEQ for Windows Version SEQ ID NO 392
LENGTH: 309
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RESULT 5
US-09-827-271-392
; Sequence 392, Application US/09827271
; Publication No. US20030165504A1
; GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 392
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APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/827,271
CURRENT FILING DATE: 2001-04-04
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                                                     EVNVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVSNTSFELNSENVTMKVVSV
                                                                                                                    DEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAFSMP 180
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LYNVTINNTYSCMIENDIAKATGDIKVTESEIKRRSHLQLLNSKASLCVSSFFAISWALL
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Pred. No. 6.5e-138;
No. Mismatches 0;
                                                                                                                                                                                                                                                                                    Score 1574; DB 10;
Pred. No. 6.5e-138;
); Mismatches 0;
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APPLICANT: Fanger, Gary R.

APPLICANT: Retter, Marc W.

ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER FILE REFERENCE: 210121.491C7

CURRENT APPLICATION NUMBER: US/10/010,742

CURRENT FILING DATE: 2001-11-30

NUMBER OF SEQ ID NOS: 307

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 209

LENGTH: 309
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; TYPE: PRT
; ORGANISM: Homo s
US-10-010-742-209
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US-10-010-742-209
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APPLICANT: Dillon, Dava-
APPLICANT: Day, Craig H.
Tiang, Yuqiu
Dayr
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Best Local Similarity
Matches 309; Conserv
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                                                                                                                                                                                                DEMERGRITAVFADQVIVGNASLRLKNVQLIDAGIYKCYIIISKGKGNANLEYKIGAFSMP 180
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                                                          LYNVTINNTYSCMIENDIAKATGDIKVTESEIKRRSHI
                                                                                                                    EVNVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVSNTSFELNSENVTMKVVSV
                                                                                                                                         EVNVDYNASSETIRCEAPRWFPQPTVVWASQVDQGANFSEVSNTSFELNSENVTMKVVSV 240
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                        PLSPYLMLK 309
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Zehentner, Barbara
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McNeill, Patricia D.
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Pred. No. 6.5e-138;
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RESULT 7
US-10-198-053-392
US-10-198-053-392
; Sequence 392, Application US/10198053
; Publication No. US20030124140A1
; GENERAL INFORMATION:

APPLICANT: Bangur,

Chaitanya

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; TYPE: PRT; ORGANISM: Homo US-09-778-320-208
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US-09-778-320-208
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; ORGANISM: Homo sapiens
US-10-198-053-392
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                 Query Match
Best Local Similarity
                                                                                                         NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 208
LENGTH: 282
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CURRENT APPLICATION NUMBER: US/10/198,053
CURRENT FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 624
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 392
LENGTH: 309
       Matches
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                                                                                                                                                          APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer
APPLICANT: Mang, TongTong
APPLICANT: Wang, TongTong
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE 'IITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.491C5
CURRENT APPLICATION NUMBER: US/09/778,320
CURRENT FILING DATE: 2001-02-06
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APPLICANT:
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Best Local
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Fanger, Gary R.
Hill, Paul
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Day, Craig H.
                                                                                                                                                                                                                                                                                                             Jiang,
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     Conservative
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ilarity 100.0%;
Conservative (
                                                                             sapiens
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90.9%; Score 1431; DB 9;
100.0%; Pred. No. 1.1e-124;
cive 0; Mismatches 0;
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APPLICANT: Abbott Laboratories
APPLICANT: Billing-Medel, Patricia A.
APPLICANT: Cohen, Maurice
APPLICANT: Colipitts, Tracey L.
APPLICANT: Colipitts, Tracey L.
APPLICANT: Russell, John C.
APPLICANT: Russell, John C.
APPLICANT: Hodges, Steven C.
APPLICANT: Klass, Michael R.
APPLICANT: Kratochvil, Jon D.
APPLICANT: Kratochvil, Jon D.
APPLICANT: Stroupe, Stephen D.
APPLICANT: Stroupe, Stephen D.
APPLICANT: Gordon, Juliano
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
TITLE OF INVENTION: DETECTING DISEASES OF THE BREAFFILE REFERENCE: 6251.US.Pl
CURRENT FILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: US 08/972,376
PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
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; LENGTH: 282
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 90.9%; Sometime 100.0%; Some
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208 WASQVDQGANFSEVSNTSFELNSENVTMKVVSVLYNVTINNTYSCMIENDIAKATGDIKV
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APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Baker David
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Patent No. US20020051990A1
GENERAL INFORMATION:
APPLICANT: OPLE, ERIC
APPLICANT: MCLACHLAN, KAREN
APPLICANT: HEARD, CHERYL J.
TITLE OF INVENTION: NOVEL GENE TARGETS AND LIGANDS THAT BIND THERETO FOR TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF OVARIAN CARCINOMAS
FILE REFERENCE: 037003-0286631
CURRENT APPLICATION NUMBER: US/09/877,065
CURRENT FILING DATE: 2001-06-11
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Patent No. Uszve-
Patent INFORMATION:
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Best Local Similarity
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PRIOR FILING DATE: 2000-06-09
NUMBER OF CONTROL OF 
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SOFTWARE: PatentIn Ver. 2.1
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J ID NO 8
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                                                                                                                     Gerber, Hanspeter
Gerritsen, Mary E.
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Fong, Sherman
                       Godowski,Paul J.
Grimaldi,J.Christopher
                                                                                        Goddard, Audrey
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CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc

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OR FILING DATE: 1997-06-16
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OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/062310
OR FILING DATE: 1997-11-12
OR APPLICATION NUMBER: 60/065311
OR FILING DATE: 1997-11-13
OR APPLICATION NUMBER: 60/065311
OR FILING DATE: 1997-11-24
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GENERAL INF
                              APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrar
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C56
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Godowski, Paul
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Kljavin, Ivar
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Gerber, Hanspeter
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Desnoyers, Luc
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NUMBER: 60/088824 NUMBER: 60/088810

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60/088734 60/088655

NUMBER: 60/088742

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NUMBER: 60/088217

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NUMBER: 60/0: 1998-06-04

60/088326 60/088033

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3: 1998-06-04 NUMBER: 60/0 3: 1998-06-04

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RESULT 14
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; Sequence 291, Application US/09989727
; Sequence US20020072497A1
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C65
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT APPLICATION NUMBER: US/09/989,727
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APPLICANT: Baker,Kevin F
APPLICANT: Botstein,Davi
APPLICANT: Desnoyers,Luc
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Roy, Margaret Ann
Stewart, Timothy A.
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Grimaldi, J.Christopher
Gurney, Austin L.
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Botstein, David
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APPLICATION NUMBER: 60/091478
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APPLICATION NUMBER: 60/090542
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APPLICATION NUMBER: 60/090254
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Search completed: May Job time : 48 secs

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CURRENT APPLICATION NUMBER: US/09/910,689
CURRENT FILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 307
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 208
LENGTH: 282
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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APPLICANT: Day, Cr
APPLICANT: Jiang,
APPLICANT: Houghto
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Patent No.
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APPLICANT: McNeill, Patricia D.
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION: DIAGNOSIS OF
FILE REFERENCE: 210121.491C6
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Mitcham, Jennifer
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Jiang, Yuqiu
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